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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 1 13:52:39 1999; MasPar time 25.13 Seconds 390.202 Million cell updates/sec Run on:

not generated. Tabular output

Description: Perfect Score:

>US-09-026-400-2 (1-461) from US09026400.pep 3223 1 MVHQSNGHGEAAAAANGKS......LERVKSFCQRNKKKNSINGC 461 Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part11 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 35.539; Variance 164.075; scale 0.217 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Pred. No.	1 560-000	7 136-252	8.258-24	4 950-13	6 000-13	3 196-09	1 730-08	30.00	1 950-03	1 959-07	1 950 07	7 570-07	2000-000	0.00	4./1e-UD	5.64e-05	5.64e-05
Description	Nicotianamine aminotr	Nicotianamine aminotr	Aquifex aspartate ami	Aquifex aspartate ami	Ammonifex degensias	Barley alanine aminot	Carnation ACC synthas	Human kvnirenine amin	Rat kvnirenine aminot	Rat kvnurenine aminot	Rat kvnurenine aminot	Rat ALT	Rose 1-aminoguelopron	ACC SINTENCE COLUMN	acc syncherase.	Poplar 1-aminocyclopr	Zucchini ACC synthase
ID	W61642	W61643	W24257	W24249	W24252	W22943	W04558	R89906	R89896	R89897	R89898	R35231	W60239	R25406	001001	WZ1/55	R15505
DB	34	34	56	56	56	56	20	17	17	11	17	7	32	C	) (	2	m
Length	461	551	394	373	398	482	517	422	423	437	457	496	480	493	1	480	493
Query Match	100.0	9.68	12.5	8.6	8.6	7.2	6.9	6.7	6.5	6.5	6.5	6.1	5.6	5.6		0	5.5
Score	3223	2888	403	277	276	231	222	216	209	209	209	195	180	179	1 1	0/1	1/8
Result No.	1	7	m	4	ស	9	7	ω	თ	10	11	12	13	14		7 .	10
	Query Score Match Length DB ID Description	Score Match Length DB ID Description P 3223 100.0 461 34 W61642 Nicotianamine aminot A	Score Match Length DB ID Description Pr 3223 100. 461 34 W61642 Nicotianamine aminotr 4. 2888 89.6 551 34 W61643 Nicotianamine aminotr 7.	Ouery Score Match Length DB ID Description P 3223 100.0 461 34 W61642 Nicotianamine aminotr 4 2888 89.6 551 34 W61643 Nicotianamine aminotr 7 403 12.5 394 26 W24257 Aquifex asonrtate amin	Query         Query         Description         Percentage           3223         100.0         461         34         W61642         Nicotianamine aminotr           2888         89.6         551         34         W61643         Nicotianamine aminotr           403         12.5         394         26         W42427         Aquifex aspartate ami           277         8.6         373         26         W42429         Aquifex aspartate ami	Query         Score Match Length DB ID         Description         P           3223 100.0         46134 W61642         Nicotianamine aminotr 4         2888 89.6         551 34 W61643         Nicotianamine aminotr 4         403 12.5         394 26 W42457         Aquifex aspartate ami 8           277 8.6         398 26 W42452         Aquifex aspartate ami 4         376 26 W2455         Ammonifex decensis as 6	Ouery Score Match Length DB ID  3223 100.0 46134 W61642 Nicotianamine aminotr 4 2888 89.6 55134 W61643 Nicotianamine aminotr 4 403 12.5 394 26 W24257 Aquifex aspartate ami 8 27 8.6 373 26 W24249 Aquifex aspartate ami 4 276 8.6 373 25 W22439 Aquifex aspartate ami 4 276 8.6 373 25 W22439 Aquifex aspartate ami 4 276 8.6 373 26 W22439 Aquifex aspartate ami 4 276 8.6 373 26 W22439 Aquifex aspartate ami 4 277 8.7 8.7 8.7 8.7 8.7 8.7 8.7 8.7 8.7 8	Ouery Courty Score Match Length DB ID Description 3223 100.0 461 34 W61642 Nicotianamine aminotr 4 403 12.5 394 26 W24257 Aquifex aspartate ami 8 277 8.6 373 26 W2429 Aquifex aspartate ami 8 276 8.6 398 26 W24294 Aquifex aspartate ami 8 27 8 25 25 8 26 W24294 Aumonifex degensii as 6 222 6.9 217 20 W04558 Carnation ACC synthss 1	Ouery Score Match Length DB ID Description 323 100.0 46134 W61642 Nicotianamine aminotr 4 2888 89.6 55134 W61643 Nicotianamine aminotr 7 323 10.5 394 26 W24257 Aquifex aspartate ami 8 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## ALIGNMENTS

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NEESULT 1
Wel642 standard; Protein; 461 AA.

Me1642 standard; Protein; 461 AA.

Me1642 standard; Protein; 461 AA.

Me1642 standard aninotzansferase 49564.15 molecular weight protein.

DE Nicotianamine aminotzansferase; plant; iron absorption;

KW nicotianamine aminotzansferase; plant; iron absorption;

KW ron deficiency chlorosis.

SG ramineae sp.

PP 8-860499-A2.

PP 8-860499-A2.

PP 19-FEB-1997; JP-037499.

PR 75UMO ) SUMITON CHEM CO LTD.

PR 75UMO ) SUMITON CHEM CO LTD.

PR 75UMO ) SUMITON CHEM CO LTD.

PR 8-439341/38.

DR N-PSDB, Well?

New nicotianamine aminotransferase protein and DNA - useful for enhancing iron absorption of plant cells

PR 19-FEB-1997; JP-03749.

PR New nicotianamine aminotransferase can be used in a plasmid to transform continuation and it is continuated (though not stated) that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be used in odetect, amplify sequence 461 AA;
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Pred. No. 4.56e-283;
0; Mismatches 0; Indels 0; Gaps
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Best Local Similarity 100.0%;
Matches 461; Conservative
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New transaminase(s) and aminotransferase(s) derived from host cells

New transaminase(s) and aminotransferase(s) derived from host cells

rused for producing enzymes, and hybridisation probes for a CDNA or

genomic library

Claim 19; Fig 10; 95pp; English.

This protein sequence comprises aspartate aminotransferase VF5/AA

Chaim 19; Fig 10; 95pp; English.

This protein sequence comprises aspartate aminotransferase VF5/AA

Chaim 19; Fig 10; 95pp; English.

Chaim 20; Agriculty pure chiral compounds used in the production of optically pure chiral compounds used in the production of optically pure chiral compounds used in the production of optically pure chiral compounds used in the production of optically pure chiral compounds used in the chaimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed enzyme. The measurement of an animed and chemical and chemical enzyme.
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HLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMGVFGHIAPVLSIGSLSKSWIVPGWR
                                                            lgwvavydprkilgetkistsitnylnvstdpatfigaalpgilentkedffkaiigllk
                                                                                                  Score 403; DB 26; Length 394;
Pred. No. 8.25e-24;
87; Mismatches 145; Indels 26;
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                                                                                                                                                                                                                                                                                                                              551
                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998 (first entry)
Aquifex aspartate aminotransferase VF5/AA.
Aspartate aminotransferase; VF5/AA; chiral compound.
                                                                                                                                                                                                                                                                                                                              gsvlgmanwvritfacvpsslqdglgriksfcqrnkkrnssddc
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M. W4257; standard; Protein; 394 AA AC W4257;
DT W4257;
DT W4257;
DT W4257;
DT W5257;
DT W5257;
DT W5257;
DE Aquifex spertate aminotransferas
Squifex sp. strain VF5.
NW W69729187-A1.
PP 14-AUG-1997; U01094.
PP 21-AN-1996; U5-56950.
PR (RECC-) RECOMBINANT BIOCATALYSIS
PR New TANDSAMINANT BIOCATALYSIS
PR NESCED-1996; U5-599171.
PR NPT: 97-415343/38.
DR N-PSDB; T78781.
PP New transaminase(s) and aminotra
PT New transaminase(s) and aminotra
PT Seed for producing enzymes, an
PT Genomic library
PT Genomic library
PT Genomic library
PT Genomic library
CC Aduifex VF5, a strictly chemo
CC Which grows optimally at 85-90 d
CC Which grows optimally at 85-90 d
CC Mich grows optimally at 85-90 d
CC C Aduifex VF5, a strictly chemo
CC Aduifex VF5, a strictly chemo
CC Aduifex VF5, a strictly chemo
CC C Aduifex VF5, a strictl
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Best Local Similarity 29.1%;
Matches 106; Conservative
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Claim 3; Page 14-15; J7pp; English.
The nicotianamine aminotransferase can be used in a plasmid to transform plant cells to produce cells with enhanced iron absorption, and it is implied (though not stated) that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be regenerated from the transformed cells. The gene fragment can be used to detect, amplify and/or isolate nicotianamine aminotransferase genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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Nicotianamine aminotransferase 58148.62 molecular weight protein.
Nicotianamine aminotransferase; plant; iron absorption;
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Pred. No. 7.13e-252;
30; Mismatches 20;
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21-FEB-1998; 102891.
21-FEB-1997; JP-037499.
(SUMO ) SUMITOMO CHEM CO LID.
MORI S, NARABIShI H, TAKAHAShI M;
WPI: 98-439341/38.
N-PSDB; V48148.
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Local Similarity 88.1%;
nes 409; Conservative
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EP-860499-A2.
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                                                                                                                                                                                                                                                                                                                                                                        genomic library

S claim 19; Fig 2: 95pp; English.

This protein sequence comprises aspartate aminotransferase B

(VFS/AAB) of Aquifex VF5, a strictly chemolithoautotrophic, marine

(Nigh Salt medium. The amino acid sequence was deduced from an

isolated genomic DNA sequence (see T78773). Claimed thermostable

transaminases and aminotransferases (W24248-57) can be produced

C from native or recombinant host cells for use with L- and/or

C from native or recombinant host cells for use with L- and/or

C b-amino acids for production of optically pure chiral compounds

used in the pharmaceutical, agricultural and other industries. A

method is claimed for transferring an amino group from an amino

c acid to an alpha-ketc acid using a claimed enzyme. The measurement

of aspartate aminotransferase levels in blood serum is used as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : || :|:|| |::| | :: | :: | :: | 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 lhisspqnptgtlyspetlkelaeyceekgmyfisdelyhglvyegrehtale-fsdra- 214
                383 MFVMVKLNLHLLEEIHDDIDFCCKLAKEESVILCPGSVLGMENWVRITFACVPSSLQDGL 442
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fyifpdfsaya-eklggdvklsefllekakvavvpgsafgapgflrlsyalseerlvegi 384
                                                                                                                                                                                                                                                                                                                                                 New transaminase(s) and aminotransferase(s) derived from host cells - used for producing enzymes, and hybridisation probes for a CDNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iv-ingfskyfcmpgfrigwmiv--peelvrkaei-v-iqnvf-isa-p-tlsqya-a--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 277; DB 26; Length 373;
Pred. No. 4.95e-13;
92; Mismatches 132; Indels 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquifex aspartate aminotransferase B (VF5/AAB).
Aspartate aminotransferase B; VF5/AAB; chiral compound.
Aquifex sp. strain VF5.
W09729187-A1.
                                                                                                                                                                                                                                                                                         (RECO-) RECOMBINANT BIOCATALYSIS INC. SWABSON RV, WALTEN PV; WPI; 97-415343/38 N-PSDB; 178773.
                                                                                                                           T 4
W24249 standard; Protein; 373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 8.6%;
Local Similarity 27.9%;
Les 98; Conservative
                                                                                                                                                                 (first entry)
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21-JAN-1997; U01094.
08-MAY-1996; US-646590.
09-FEB-1996; US-599171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 AA;
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Matches
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14-AUG-1997.
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80-MAY-1996; US-646590.
80-FEB-1996; US-599110.
87-8-1996; US-599110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Barley alanine aminotransferase.
Alanine aminotransferase; barley; Brassica tugor gene - 26;
Alanine aminotransferase; barley; Brassica tugor gene - 26;
Barley & Gene; promoter; osmotic & Stress; stress tolerance; drownitrogen assimilation; nitrogen metabolism; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 276; DB 26; Length 398
Pred. No. 6.00e-13;
69; Mismatches 124; Indels
                                                                                                                                                                               Ammonifex degensii aspartate aminotransferase KC4/AA.
Aspartate aminotransferase; KC4/AA; chiral compound.
Ammonifex degensii strain KC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oilseed rape; rapeseed oil; canola.
Hordeum vulgare.
W09730163-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 aaalaalkgpqepvenmrrafqkr 300
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T 5
W24252 standard; Protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.6%;
Best Local Similarity 23.9%;
Matches 63; Conservative
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1997.
14-FEB-1997; CA0100.
                                                                                                                                    18-FEB-1998
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403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                   reneric construct iot expressing enzyme involved in illicogen assimilation or metabolism in plants - useful to improve stress tolerance, reduce fertiliser demand or increase growth rate tolerance, reduce fertiliser demand or increase growth rate tolerance, reduce fertiliser demand or increase growth rate is example 3; fig 5; 45pp; English.

This protein comprises barley alanine aminotransferase, an enzyme involved in alanine biosynthesis and nitrogen metabolism. A claimed genetic construct (A) for expression in plants comprises a sequence encoding an enzyme involved in nitrogen as the casimilation/metabolism, and an inducible promoter (see T75571).

Also new are: (1) a cloning, expression or plant transformation vector containing (A); and (2) a plant cell transformed with (A), and a plant regenerated from it. (A) is used to transform rape, and a plant regenerated from it. (A) is used to transform rape, containing (A); and (2) a plant cell transformed with (B); cresulting in improved agronomic properties, e.g. better stress continue and in improved agronomic properties, storage or metabolism of nitrogen. The btg-26 promoter was demonstrated to induce over-expression of barley alanine aminotransferase in transgenic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 yshsqgikglrdaiasgiasrdgfpanaddifltdgaspgvhlmmqllirnekdgilvpi 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 YAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAGGTQAIEVIIPVLAQTAGANILLPR 175
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Carnation cv. White Sim 1-aminocyclopentane-1-carboxylic acid (ACC)
synthase (W04558) catalyses the initial step of ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing transgenic plants, with reduced climacteric ethylene produ. - to give flowers and buds, specifically carnations, with increased post-harvest life
                                                                                                                                                                                                                         Genetic construct for expressing enzyme involved in nitrogen assimilation or metabolism in plants - useful to improve stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carnation; 1-aminocyclopentane-1-carboxylic acid sy ACC synthase; co-suppression; ethylene; senescence; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michael MZ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 231; DB 26;
Pred. No. 3.19e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 tggvlaeengydivkfckneglvlladevy 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALLR-) ALLRAD NO 1 PTY LTD. (FLOR-) FLORIGENE INVESTMENTS PTY LTD. Cornish EC, Graham MW, Gutterson NI,
                                                                                                                                                    Stroeher VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%;
Best Local Similarity 30.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carnation ACC synthase.
US-599968.
                                                (UYAL-) UNIV ALBERTA.
(GODD/) GODD A G.
(MUEN/) MUENCH D G.
GODD ASTROPHER V L.
GOOD AG, MUENCH DG, S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-1996; AU0286.
09-MAY-1995; AU-002862.
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                                                                                                                                                      Good AG, Muench DC
WPI; 97-425038/39.
N-PSDB; T75572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 AA;
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     14-FEB-1996;
14-FEB-1996;
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383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 vldkdtlkmlltfýnak-nihlvcdeiyattvfnspsfisvaevikdmphvngdlvhily 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 glpefrsavakfmgkardekvifnpdrivmsggassasetllfclan-pgdaflipspyyp 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 afnrðlrwrtgvnlipftcsssnnfkitkealgsayedalkknikvkgiivtnpsnplgt 214
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                                                                                                                                                                                                                                                                                                                                       Score 222; DB 20; Length 517;
Pred. No. 1.73e-08;
91; Mismatches 136; Indels 33; Gaps
biosynthesis in the plant. Its amino acid sequence was deduced from a full-length gene (T38896). Expression of a nucleic acid (T38897) coding for a fragment (W04559) of the ACC synthase in transgenic carnation reduces the formation of ACC synthase by co-suppression. The reduction in ACC synthase activity results in decreased climacteric ethylene prodn. by the plant and hence delayed senescence of flowers and buds after cutting, and increased post-harvest_life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 lwrviinevkinvspgssflcsepgwfrvcfanmdnatldvalnrirsfvtrgrvdns 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human kynurenine aminotransferase (KAT).
Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
KYN; brain; NMDA receptor; glutamatergic function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FCCKLAKEESVILCPGSV-LGME-NWVRITFACVP-SSLQDGLERVKSFCQRNKKNNS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 NYEARAAFNK-LEVRHFDLIPDKGWEIDIDSLESI-AD---KNTTAM-VII-NPNNPCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 slskdmgmpgfrvgiiysyn-drvvstarrmssf-g-l-vssg-tqfmlaallsdddfvr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R89906 standard; Protein; 422 AA.
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23-JUN-1995: U07855.
07-JUL-1994: US-271667.
(PRAA.) PHARMACIA SPA.
(UYMA-) UNIV MARYLAND BALTIMORE.
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                                                                                                                                                                                                                                                                                                                                                      Match 6.9%;
Local Similarity 27.4%;
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15-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            98; Conservative
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                                                                                                                                                                                                                                                                                   517 AA;
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Schwarcz

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168 lgasndwqldpaelaskftprtkvlvlntpnnplgkvfsrmelelvanlcqqhdvvcisd 227
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Sequences encoding Kynurenine aminotransferase (KAT) can be inserted into vectors and subsequently cells and hence can be used for gene therapy. The vector and host cells can be used for cerebral implantation to where KAT can directly catalyse the production of kynurenic acid (KYNA) from kynurenine (KYN). It is thought KNA acts as a negative endogenous modulator of cerebral glutamatergic function. KYNA concentrations and the activity of KAT show an increase with age. AT inhibitors, by providing an increase of the slutamatergic tone at the NWDA receptor, could be useful in situations where NWDA receptor function is insufficient and/or KAT.
                                                                                                                                                                                                                                                                                                                                Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) - useful in gene therapy applications and for identifying KAT in brain
         Rat kynurenine aminotransferase (KAT) clone.
Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
KYN; brain; NMDA receptor; glutamatergic function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity and KTNA levels are abnormally enhanced. Hence they could be particularly useful in the treatment of the pathological consequences associated with the aging processes in the brain. Three KAT clones are described in 711560, 711742-43.
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KYN; brain; NWDA receptor; glutamatergic function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 6.5%; Score 209; DB 17; Length 437; Local Similarity 33.0%; Pred. No. 1.95e-07; Nes 35; Conservative 24; Mismatches 46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 EVYGKLVLGSAPFIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWV 301
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Rat Kynurenine aminotransferase (KAT) clone.
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                                                                                                                     25-JAN-1996.
23-JUN-1995; UO7855.
07-JUL-1994; US-271667.
(PHAA ) PHARNACIA SPA.
(UYMA-) UNIV MARYLAND BALTIMORE.
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23-JUN-1995; UO7855.
07-JUL-1994; US-271667.
(PHAA ) PHARNACIA SPA.
(UYMA-) UNIV MARYLAND BALTIMORE.
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                                                                                                                                                                                                                                                                                     WPI; 96-097623/10.
N-PSDB; T11742.
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N-PSDB; T11743.
                                                                                 rattus.
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WO9601893-A1.
                                                                                                    WO9601893-A1.
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                                                                                                                                                                                                              iqngelgsssnwqldpmelagkftsrtkalvlntpnnplgkvfsreelelvaslcqqhdv 208
                                                                                                                                                                                                                                             192 VRHFDLIPDKGWEIDIDSLESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 lgasndwgldpaelaskftprtkvlvlntpnnplgkvfsrmelelvanlcgghdvvcisd 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 LIPDKGWEIDIDSLESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGILVIAD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences encoding yourselve and be used (KAI) can be inserted into vectors and subsequently cells and hence can be used for gene therapy. The vector and host cells can be used for cerebral implantation to where KAI can directly catalyse the production of kynurenic acid (KYNA) from kynurenine (KYNN). It is thought KYNA acts as a negative endogenous modulator of cerebral glutamatergic function. KNA concentrations and the activity of KAI show an increase with age. KAI inhibitors, by providing an increase of the silutanians where NMDA receptor, could be useful in situations where NMDA receptor function is insufficient and/or KAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) - useful in gene therapy applications and for identifying KAT in brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
KYN; brain; NMDA receptor; glutamatergic function.
consequences associated with the aging processes in the brain. This is the human RAT sequence. Three rat KAT clones are described in Tili560, Tili742-43. Sequence 422 AA;
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Pred. No. 1.95e-07;
24; Mismatches 46; Indels
                                                                                                                       Length 422;
                                                                                                                Score 216; DB 17; Length 42
Pred. No. 5.30e-08;
29; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                : |:|||| :| :||:||| IVIADEVYGKLVLGSAPFIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWV
                                                                                                                                                                                                                                                                                                 209 vcitdevyqwmvydghqhisiaslpgmwertltigsagktfsatgwkvgwv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat kynurenine aminotransferase (KAT) clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Figure 2; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    л 9
R89896 standard; Protein; 423 AA.
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R89897 standard; Protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAA ) PHARMACIA SPA. (UYMA-) UNIV MARYLAND BALTIMORE.
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                                                                                                                  Similarity 30.6%;
34; Conservative
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Local Similarity 33.0%;
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07-JUL-1994; US-271667.
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                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 lgasndwqldpaelaskftprtkvlvlntpnnplgkvfsrmelelvanlcqqhdvvcisd 247
kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts as a negative endogenous modulator of cerebral glutamatergic function. KYNA concentrations and the activity of KAT show an increase with age. KAT inhibitors, by providing an increase of plutamatergic tone at the NWDA receptor, could be useful in situations where NWDA receptor function is insufficient and/or KAT be particularly useful in the treatment of the pathological consequences associated with the aging processes in the brain. Finee KAT clones are described in T11560, T11742-43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In diagnosing heart diseases
Disclosure; Page 11-13; 15pp; Japanese.
The sequences given in R35230-31 represent human and rat alanine
aminotransferase (ALT) genes respectively. ALT is an important
marker in the diagnosis of hepatic disease. Gene fragments of ALT
can be used in inexpensive, large scale production of human ALT
which can then be used as a standard in the determination of human
Serum ALT. See also Q40500-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer; polymerase chain reaction; PCR; amplify; human; diagnosis; alanine aminotransferase; ALT; marker; hepatic disease; serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alanine-amino-transferase gene fragments - used as marker
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                                                                                                                                                                                                                              Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 195; DB 7; Length 496;
Pred. No. 2.57e-06;
42; Mismatches 56; Indels
                                                                                                                                                                                                                          Score 209; DB 17; Length 45
Pred. No. 1.95e-07;
24; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                           248 evyqwlvydghqhvsiaslpgmwdrtltigsagksfsatgwkvgwv 293
                                                                                                                                                                                                                                                                                                                                                                                                  257 EVYGKLVLGSAPFIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWV 301
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Rose 1-aminocyclopropane-1-carboxylase synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1991; 222318.
06-AUG-1991; UP-222318.
(K-AAG.) JRAGAKU OYOBI KESSEI RYOHO KENKYUSHO.
(WPI; 93-136892/17.
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W60239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 12
R35231 standard; Protein; 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.1%;
Best Local Similarity 29.2%;
Matches 45; Conservative
                                                                                                                                                                                                                            Query Match 6.5%;
Best Local Similarity 33.0%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R35231;
10-AUG-1993 (first entry)
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J05068548-A.
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New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced T rose, used to develop products for producing plants with reduced T rose, used to develop products for producing plants with reduced T claim 60; Fig 10: 77pp; English.

Claim 60; Fig 10: 77pp; English.

This amino acid sequence of this 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) of rose cv. Red Cardinal was deduced from isolated cDNA clone pRosekac7 (see V30330). The invention relates to new isolated ACC synthase genes from geranium and rose (see V30324-26 and V30330) and the use of antisense fragments of these genes to control expression of ACC synthase genes in transgenic plants, especially in geranium, rose and woody plants. By reducing the amount of ACC synthase produced in plant cells, the rate of ACC conversion to ethylene can be decreased. This can be used to prolong the shelf-life of cut flowers and to reduce leaf yellowing and sequence 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The protection of the protecti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 lads-gnaflvpapyypgldrdvkwrtgveiipvpcrsadkfnlsitaldrafngakkrg 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 vkvrgiiisnpsnpggslltreslynlldfareknihiisnelfagstygseefvsma 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 AMV---II-NPNNPCGSVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-aminocyclopropane-1-carboxylic acid synthetase; detriment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 480;
ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
ethylene; transgenic plant; wilting; rose; pRoseKacc7.
Rosa sp. cv. Red Cardinal.
W09814465-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 180; DB 32;
Pred. No. 3.93e-05;
50; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ethylene; growth; maturity; aging; plant.
Cucurbita maxima.
                                                                                                                                                                                                                                                                               01-OCT-1996; US-724194.
(COLS ) UNIV COLORADO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
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R25406 standard; Protein; 493
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31-0CT-1990; JP-296943.
(SUMO ) SUMITOMO CHEM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 5.6%;
Local Similarity 27.0%;
les 48; Conservative
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                                                                                                                                                                                                                                30-SEP-1997; U17644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92-253389/31.
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N-PSDB; Q25896
                                                                                                                                                                                           09-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                        Ranu RS;
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              NAME OF THE PROPERTY OF THE PR
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This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase encoded by a cDNA clone isolated from poplar trees which had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone for 6 hours after one hour acclimation at 25 degrees C, 70 % relative humidity, 30 k lux and air current 30 cm/second. The gene will be useful for breeding air pollutant ozone-resistant trees, especially
                                                                                                                                    215
                                                                                                                                                                                             \verb"ttydrdtlktlvtfvnghdihlicdeiysatvfkaptfisiagiveemehckkelihilg" 275
                                                             glpefrngiasfmgkvrggrvqfdpsrivmgggatgasetvifclad-pgdaflvpspyy 155
                                                                                     231
                                                                                                                                                                                                                                                            276 slskdmglpgfrvgilysyndv-vvrrargmssf-g-l-vssqtqhllaamlsd--edfv 329
                                                                                                                                                                                                                                                                                 330 dkflaenskrlaerharftkel-dkmgitclnsnag-vfvwmdlr-rilkdqtfkaemel 386
                                                                                                                                                                                                                                                                                                                                                                   403
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                                                                                                                             aafdrdlkwrtraqiirvhcnssnnfqvtkaaleiaykkaqeanikvkgviitnpsnplg
                                                                                                                                                       32 SVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMG--V--FGHIAPVL-SIG-
                                                                                                                                                                                                                                                                                                                                                    346 ADFFRRIIGLLKESSEICYREIKENKYITCPHKPEGSMFVWYKLNLHLL-EE-1HDDIDF
                                                                                                                                                                                                                                                                                                                                                                                           387 wrviinevklnvspgssfhvtepgwfrvcfanmddntvdvalnrihsfvenidkke 442
                                                                                                                                                                                                                                                                                                                                                                                                                (Note: Record has been revised in order to correct the Organism Source field).
                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178; DB 23; Length 486;
Pred. No. 5.64e-05;
98; Mismatches 143; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1997 (revised)
26-AUG-1997 (first entry)
Poplar l-aminocyclopropane-1-carboxylic acid synthase PNACCS2.
Ozone, induction; exposure, resistance; transgenic plant; ACC;
1-aminocyclopropane-1-carboxylic acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
 Score 179; DB 5; Length 493;
Pred. No. 4.71e-05;
95; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .r 15
W21755 standard; Protein; 486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Populus nigra.

J09075088-A.

25-MAR-1997.

07-SEP-1995; 254510.

(TOYT ) TOYOTA JIDOSHA KK.

WPI: 97-239270/22.
Query Match 5.6%;
Best Local Similarity 24.7%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.5%;
Best Local Similarity 24.5%;
Matches 88; Conservative
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26-AUG-1997
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179

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ttldretlkcllsfineknihivcdeiyaatifssqnfvsvsevieevmdcnrdlihivy 269
                    324 edflaesskrikkrhgiftkgleqig-iscleskag-lfvwmnlr-hlikeqtndgemel 380
                                                                                                                                                346 ADFFKRIIGLLKESSEICYREIKENKYITCPHKPEGSMFVMVKLNLHLL-EEIHD-DIDF 403
                                                                                                                                                                             381 wrvivndvklnvspgssfhcvepgwfrvcfanmddetlevalkrihafvgegkeretls 439
                                                                                                                                                                                               slskdmglpgfrvgivysynda-vvncgrkmssf-g-1-vssq-tqyllasmlsd-eefv
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Search completed: Fri Oct 1 13:53:16 1999 Job time : 37 secs.

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Release Copyric	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
MPsrch_pp prote	protein - protein database search, using Smith-Waterman algorithm
Run on:	Fri Oct 1 13:50:56 1999; MasPar time 33.04 Seconds
Tabular output not generated.	
Title: Description: Perfect Score: Sequence:	>US-09-026-400-2 (1-461) from US09026400.pep 3223 1 MVHQSNGHGEAAAAANGKSLERVKSFCQRNKKKNSINGC 461
Scoring table:	PAM 150 Gap 11
Searched:	179066 seqs, 54579741 residues
Post-processing:	Post-processing: Minimum Match 0% Listing first 45 summaries

# Statistics: Mean 49.304; Variance 91.106; scale 0.541

sptrembl9
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

CHINATIO	Query Match Length DB ID Description Pred. No.	39.6 389 10 049451 TYROSINE TRANSAMINASE- 2.31e-248	22.5 464 5 Q93703 F42D1.2 PROTEIN. 1.33e-125	-	14.3 402 2 086587 PUTATIVE AMINOTRANSFER 3.71e-68	v	13.5 404 2 P71348 ASPARTATE AMINOTRANSFE 6.69e-63	~	394 2 (					11.2 397 2 053870 PUTATIVE AMINOTRANSFER 1.41e-47	382 2		10.0 379 1 028151 ASPARTATE AMINOTRANSFE 7.02e-40	~	.2	C C C C C C C C C C C C C C C C C C C
dР	Query Match Length DB	39.6 389 10		-	8	v		7										~	2	205
	Score	1275	726	495	460	439	435	410	403	401	374	368	2 365	361		15 330	323			

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENILVPHPGFPLYSTLCRPHNIVDKPYKIDMTGEDVR-IDLSYMATIIDDNTKAIIVNN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGNPTGGVFTKEHLEEILAFAHQYKLIIIADEIYGDLVYNGATFYPLASLSPKVPIITCD 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 SLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 VLPQSAHSKNTVNPVR-KIADACAVPPHPEKKVIKLHLGDPSVGGKLPPSEIAVQAMHES 103
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EAMADENTVAMVIINPNNPCGNVYSYDHLKKVAETAKKLGIMVITDEVYCQTIFGDKPFV 251
                                                             PMGEFSSITPVITLGGISKGWIVPGWRIGWIALNDPRGILKSTGMVQSIQQNLDITPDAT 311
                                                                              MEDINE: 94150718
MEDINE: 94150718
MELSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A.,
GRARTON M., DEAR S., DU Z., DURRIN R., FAVITON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER L., JIER M., JOHNSTON L.,
LIGHTING J., LLOYD C., MCMORRAY A., MORTINORE B., O CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THERRY MIEG J., THOMAS K., VADDIN M., VAGHARAN E.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                           312 TIVQAALPEILGKANKELFAKKNSMLKQNVELVCDR-LKEIPCLVCNKKPESCTYLLV 368
                                                                                                                                          EUKARYOTA, METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                 LIGHTNING J.; SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.5%; Score 726; DB 5; Le 30.4%; Pred. No. 1.33e-125; rative 121; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; E1346662; -. 464 AA; 51031 MW; A2E3EAB3 CRC32;
                                                                                                                                                                                                                           464 AA.
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01-FEB-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                       CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        F42D1.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z81081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 AGWLAITGP-KEHASSFIE-GIGLLANMRLCPNVPAQHAIQVALGGHQSIEDLVLPGGRL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEQRDIAWTKLNEIPGVSCV-KPAGALYAFPRLDPEVYD-IDDDEQLVLDLLLSEKILVT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 -LSARRAVVTRYELVPGFP-RFDVDDVYLGNGVSELITMTLQALLDN-GDQVLIPSPDYP 155
MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "An integrated map of the genome of the tubercle bacillus,
Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-H37RV;
BADLINE; 96181548.
PHILIPP W.J., POULET S., EIGIMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 IRGPVHQHAARLEAEGHR-ILKLNIGNPAPF-GFEAPDVIMRDIIQALPYAQGYSDSQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILTQMVDLARKHQLLLLADEIYDKILYDDAKHISLASIAPDMLCLTFNGLSKAYRVAGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 LWTASTSLAGGTPVHY-LCDETQGWQPDIADLESKITER-TKALVVINPNNPTGAVYSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 429;
                                                        NLIREESVF-CLPGQAFSAPGYFRVVLTCGSEDMEEAALRIREFCYRN 441
                                                                                                                                                                                                                                                                                                  OLIVER K., HÀRRIS D.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                     PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL; 297991; E330321; -.
PFAM; PF00155; aminotran.l.; 1.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 429 AA; 47350 MW; 9B68011A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.44e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                        AA
                                                                                                                        429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.5%;
Matches 107; Conservative
                                                                                                                                                                                           ASPARTATE AMINOTRANSFERASE. MTCY279.04C.
                                                                                                                          PRELIMINARY;
                                                                                                                                                  01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
                                                                                                                                                                               01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           STRAIN-H37RV;
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                                                                                                            3 33267
033267
033267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASVEESGPRPVLPLAHGDPSVFPARTAVEAEDAVAAALRIGQFNCYAAGVGLPAARSA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 VAQRY-QALGLEVDVDDVFLGNGVSELISMAVQALLE-DGDEVLIPAPDFPLWTAVTTLA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGKAVHY-LCDEQAEWYPDLADMEAKITDR-TKAVVIINPNNPTGAVYPKEIVEGILDLA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRHGLMVLADEIYDQILYDDAVHHSAASLAPDLVVLTFCGLSKTYRVAGFRSGWLVVTGP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 KQHARDYLEGLIMLASMRLCANAPAQYAIQAALGGR-QSIR-EL-TAPGGRLHEQRDVAW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TKILEKTKISTSITNYLNVSTD-PATF-VQEALPKILENTKADFFKRIIGLLKESSEICY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ANALEEAG-HSVLRLNTGNPALF-GFEAPEEIVQDMIRMLPRAH-G-YIDSRGILSARRA 79
                                                                                                                                                                                                                                                                                                                                                                 REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;

"A set of ordered cosmids and a detailed genetic and physical map in the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

MOL. MICROBIOL. 21:77-96(1996).

EMBL; ALO31514; E1319222; -.

TRANSFERASE; AMINOTRANSFERASE.

SEQUENCE 402 AA; 44448 MW; 185FB18E CRC32;
                                                                                                                                                         STREPTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 14.3%; Score 460; DB 2; Length 402; Local Similarity 27.7%; Pred. No. 3.71e-68; les 94; Conservative 96; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                B.G., RAJANDREAM M.A.;
TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                               TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
1D 05904 PRELIMINARY; PRT; 401 AA.
1D 059044.
DI 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 REIKENKYITCPHKPEGSMFVMVKLNIHLLEEHHDDIDF 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 EKLNEIPGISCV-KPKGALYAFPRID-PAVHKIHDDERF
                                                                         402 AA
                                                                                                CREATED)
                                                                         PRT;
                                                                                           01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, 01-NOV-1998 (TREMBLREL. 08, PUTATIVE AMINOTRANSFERASE.
                                                                         PRELIMINARY;
                                                                                                                                                                                                                     STRAIN=A3(2);
OLIVER K., HARRIS D.;
SUBMITTED (SEP-1998);
                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
PARKHILL J., BARRELL
SUBMITTED (SEP-1998)
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
MEDLINE; 97000351.
390 QGT 392
                        417 PGS 419
                                                        Query Match
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Matches
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STRAIN-OT3;
MEDLINE; 98344137.
KAWARABASIS.
Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHABAII T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 REKEKNGVDITPDDVRVTAAVTEALQLIFGALLD-PGDEILIPGPSYPPYTGLVKFYGGK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 VRHFDLIPDKGWEIDIDSL-ESIADKNTTAMVIINPNPCGSVYSYDHLAKVAEVARKLG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                PYROCOCCUS HORIKOSHII.
ARCHAEA; EURXARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95350630.
FLEISCHAMN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., FLEISCHAMN R.D., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKELAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., SCOTT J.D., SHIRLEY R., LIU D.I., GLODEK A., KELLEY J.M., STOTT J.D., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SADDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 LEKKGIK-VIRLNIGDPVKF-DFQPPEHMKEAYCRAIQEGH-NYYGDSEGLIELREAIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 PVEYRTIEEEGWQPDIDDLRKKISER-TKAIAVINPNNPTGALYDKKTIEEIINVAGEHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 SEVREAIDKLARIRICPNTPGQFA--ALAG-LIGSM-DYLKEYMKKLKERRDFIYKRLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 LVVLSDEIYDLMTYEGKHISP-GSLIKDVPVIVMNGLSKVYFATGWRLGYMYFVDPEGKL
                                                                                                                                                                                                                                                                                                                                                   "Complete" Sequence and Gene Organization of the Genome of a
Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3.";
DAN RES. 5:55-76(1998).
EMBL; APONOOG; D103131; -.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 401 AA; 45564 MW; 01CD3533 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.0%; Pred. No. 9.70e-64;
Matches 90; Conservative 83; Mismatches 135; Indels 1
09, LAST ANNOTATION UPDATE) ASPARTATE AMINOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02, CREATED)
02, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 NKYITCPHKPEGSMFVMVKLN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 IPGIS-TTKPQGAFYIFPRIE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DT1348 PRELIMINARY;
P71344; O1-FEB-1997 (TREMBLREL. 0
01-FEB-1997 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
N-1999 (TREMBLREL.
LONG HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                    SEQUENCE FROM N.A.
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ESCHERICHIA.
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                                                                                                                                                                                                                                                                                                                                                    FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENLAVAGE A.R., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIELEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRAANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 IRGPVHKEALRLEEEGNK-ILKLNIGNPAPF-GFEAPDEILVDVLRNLPSAQ-G-YCDSK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : |:|| ::::|||:| |:: |:|| | |: |:|| | |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IRAIRYKISASVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRTGQFNCYAAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYSARKAIVQYYQSKGI-LGATVNDVYIGNGVSELITMAMQALLN-DGDEVLVPMPDYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 LWTAAVTLSGGKAVHY-LCDEDANWFPTIDDIKAKVNAKTKAIVIINPNNPTGAVYSKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQEIVEIARQNNLIIFADEIYDKILYDGAVHHHIAALAPDLLTVTLNGLSKAYRVAGFRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEQRNKAYDLITQIPGITCV-KPMGAMYMFPKIDVKKFN-IHSDEKMVLDLLRQEKVLLV
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BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Mismatches 159; Indels 16;
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                              "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd ^{\prime\prime},
                                                                                                                                                                                              BROWN N.P., HAYES W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U32714; G1573250; -.
PPRAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 404 AA; 45160 MW; 8082209D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
FROM BASES 2401667 TO 2412529
(SECTION 208 OF 400) OF THE COMPLETE GENOME (SECTION 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VENTER J.C.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 435; DB 2;
Pred. No. 6.69e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405
                                                                                                                                                                SEQUENCE FROM N.A.
L TARUSON R., MUSHEGIAN A.R., BORK P.,
BORDODOVSKY M., RUDD K.E., KCONIN E.V.;
CURR. BIOL. 6:279-291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.5%;
Best Local Similarity 28.2%;
Matches 102; Conservative
                                                                                                  SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VENTER J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
P77727
P77727;
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AIRA H., BARA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KIM S., KIMORA S., KIMARIMO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
NASHIMOTO H., TOHOTO Y., WADA C., YAMAMOTO Y., YANO M.;
SUBMITIED (JAN-1997) TO EMEL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000318; G1788627; -
EMBL; AE000318; G1788627; -
EMBL; AE000318; G1788627; -
EMBL; AE000318; G1788627; -
EMBL; AENOWERSERSE; AMINOTRANSFERASE.
SEQUENCE 405 AA; 45517 MW; DF062CD9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 GLYSARKAIMQHYQARGMR-DVTVEDIYIGNGVSELIVQAMQALLNS-GDEMLVPAPDYP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMEIVEIARQHNLIIFADEIYDKILYDDAEHHSIAPLAPDLLTITFNGLSKTYRVAGFRQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.11e-57;
94; Mismatches 154; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 IRGPVLKEAKRLEEEGNK-VLKLNIGNPAPF-GFDAPDEILVDVIRNLPTAQ-G-YCDSK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ъ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWMVLNGPKK-HAKGYIEGLEMLASMRLCANVPAQHAIQTALGGY-QSI-SEFITPG-GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYEQRNRAWELINDIPGVSCV-KPRGALYMFPKIDAKRFN-IHDDQKMVLDFLLQEKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 405;
                                         BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
                                                                                         SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EMBL; AE000766; G2984217; -.
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 394 AA: 43777 MW; B9DB3011 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; STREPTOMYCES ACTINOMYCETACEAE; STREPTOMYCES
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   the hyperthermophilic bacterium Aquifex
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Pred. No. 8.18e-56;
94; Mismatches 152; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394;
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TERCERO J.A., ESPINOSA J.C., JIMENEZ A.;

TERCERO J.A., ESPINOSA J.C., JIMENEZ A.;

State of the Lysk is transcriptional requiators."

SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL: AJ006517; E1318411; --

EMBL: AJ005198; E1318407; --

TRANSFERASE; AMINOTRANSFERASE.

SEQUENCE 402 AA; 44414 MW; 5CD3256A CRC32;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3.15e-56;
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01-NOV-1998 (TREMBLREL. 08,
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Local Similarity 29.1%;
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SOLUTE-BINDING SIGNATURE AND MITOCHONDRIAL SIGNATURE PROTEIN (ASPB)
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                                                                                                                                              HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
HELICOBACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the gastric pathogen Helicobacter pylori[published erratum appears in Nature 1997 Sep 25.389(649):412].";
NATURE 388:539-547(1997).
EMBL; AE000580; G2313794; -.
                                                                                                             VAQRYQALGLD-EVSVDDVFLGNGVSELVTMAVQALLE-DGDEILIPAPDFPLWTAVTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QHARDYLEGLIMLASMRLCPNAPAQFAIQAALGGR-QSIR-EL-TAPGGALHEQRDRAWE
                                                                                                                                                                                                                                                               RHGLMVFADEIYDQILYDDAVHHSVAALAPDLVVLTFCGLSKTYRVAGFRSGWLVITGPR
24 ANALEEAG-HSVLRLNTGNPALF-GFEAPEEIVQDMIRMLPQAH-G-YTDSRGVLSARRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDFDTPQAIKDAAIKALNDG-FTKYTPVAGIPELLKAIAFKLKKENNLDYEPNEILVSNG
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Pred. No. 3.06e-50;
85; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42874 MW; BAD53859 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.6%; Score 374;
larity 26.7%; Pred. No. 3
Conservative 85; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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PFAM; PF00155; aminotran_1; 1.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 AA;
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les: 97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-26695;
MEDLINE; 97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 WPR 369
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KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
A ZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELL S.C., BRON S.,
BROUTLLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
A GHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
DENIZOT F., DEVINE K.M., DUSTERHOFT A., EPRICHE S.D., EMMERSON P.T.,
RITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALIERON N.,
A GHIM S.Y., GLASER P., GOFFEAN A., GOLIGHTLY E.J., GRANDI G.,
A GUISEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
A HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
A KURTA K., LEVIER P., KONINGSTER BLANGHARD M.,
KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
A MOONE D., O'REILLY M., CGAWA K., OGIWARA A., OUDGAR B., PARK S.H.,
PARRO V., POHL T.M., POSTFELLE B., RARPONDLIK S., PRESCAT A.M.,
PRESCAN E., PUNIC P., WILLUM M., MELLADO R.P., MISULLE B., RARPONDLIK S., PRESCAT A.M.,
PRESCAN E., PUNIC P., PURILLE B., RARPONDLIK S., PRESCAT S.,
RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
A RIEGER M., RIVOLTA C., ROCHE B., ROSE M., SADAIE Y.,
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152 GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKG-WEIDIDSL 210
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                                                                                                                                                                                                                                                                                         VSCAAVSEEMKKRTITISGLSKSVAMTGWRMGYAASKDKKLVKLMNNLQSQCTSNINSIT
                                                                                               KDALSPK-TKMLILTTPSNPTGMLYSKAELEVLGEVLKDTKVWVLSDEIYEKLVY-KGEF
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BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168;
OUDEGA B., KONINGSTEYN G.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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DANCHIN A.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL 39.5 KD PROTEIN.
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MEDLINE; 98044033.
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SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
SEKIGUCHI J., SEKOMSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDO B.
SOROKIN A., TACCONI E., TARAGI T., TAKAHASHI H., TAKEMARU K.,
TAKENCHI M., TAMAKOSHI A., TAMAKA T., TERRSTRA P., TOGNONI A.,
TOGATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTI A.,
VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENBGGR T.,
WINDERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
TOGHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
SUDTILIS.",
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KATARMA M., SAKAI Y., OKAMOTO S., IHARA F., NIHIRA T., YAMADA Y.;
KATARMA M., SAKAI Y., OKAMOTO S., IHARA F., NIHIRA T., YAMADA Y.;
"Gene organization in the ada-rpli region of the Streptomyces
virginiae chromosome.";
SUBMITTED (MAX-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-! COFACTOR: PYRIDONAL PHOSPHATE (BY SIMILARITY).
-! COFACTOR: PSELONGS TO CLASS-I OF PYRIDONAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                        KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 DFEAAVTEKTKAILICSPSNPTGSVYSKEELNEIAEFAKKHDVIVLADEIYAELTYDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; STREPTOMYCES STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                          -I SIMILATARIA.

MINOTRANSFERAGES.

EMBL; 29934; E311527; -.

EMBL; 299120; E1184218; -.

PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.

PPRAM; FF00155; aminotran_1; 1.

HYPOTHETICAL PROTEIN; PYRIDOXAL PHOSPHATE.

247 AA: 39461 MW; FD6B02F9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.20e-49;
59; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9240ED06 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 FIPMGVF-GHIAPVLSIGSLSKSWIVPGWRLGWVA 302
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PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
PRAM; PF00155; aminotram_1; 1.
TRANSFESSE; PYRIDOXAL E
SEQUENCE 397 AA; 42381 MW; 9240ED06 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 29.8%;
Matches 64; Conservative
                                                                                                                                                                                                       NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREPTOMYCES VIRGINIAE.
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q60013;
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                                                                                                                     81 RDSGYEVEASQVLVTNGGKQAIXEAFAAIL-D-PGDEVIVPAPYWTTYPESIRLAG-GVP 137 : | : | : | | | : | : | : | | : |
                                                                                                                                                                                   138 -VDVVADETTGYRVSVEQLEAARTERTKVVLFVSPSNPTGSVYSEADAKAIGEWAAEHGL 196
                                                                                                                                                                                                                                                197 WVLTDEIYEHLVYGEAKFTSLPVLVPALRDKCIIVNGVAKTYAMTGWRVGWY-IAPQDVI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: |||: :: |:| || :: |:| || | | :: |::: ||| ::|:| 75 SGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRTGQENCYAAGVGLPAARSAVAEHLS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 IEPFYDSYSPVVAMAGAHRVTVPLVPDGRGFALDADALRRAVTPRTRALIINSPHNPTGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 YPPGPGSAPLRRAIAAQRRRHFGVDYD-PETEVLVTVGATEAIAAAVLGLVE-PGSEVLL 114
                                                           25 AAGRPVIGFGAGEPD-FPT-PDYI-VEAAVEAC-RNPKYHRYTPAGGLPELKAAIAAKTL 80
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLE S.T.; "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                  256 KAAINLQSHAISNVSNVAQVAALAAVSGNLDAVAEMRKA-FDRRRQIMVKMLNEI 309
Score 365; DB 2; Length 397;
Pred. No. 2.14e-48;
76; Mismatches 118; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BARRELL B.G., RAJANDREAM M.A. EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EMBL; RAL022004; E1254000; -.
TRANSTEALSE; AMINOTRANSFERSE.
SEQUENCE 397 AA; 42209 MW; 447498CB CRC32;
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01-JUN-1998 (TREMBLREL. 06,
01-JUN-1998 (TREMBLREEL. 06,
01-OV-1998 (TREMBLEEL. 08,
PUTATIVE AMINOTRANSFERASE.
Query Match 11.3%;
Best Local Similarity 28.5%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYCOBACTERIUM TUBERCULOSIS
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MEDLINE; 96181548.
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053870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 HTH-YADQRGLRELRAALAARLPERPGGAWDADDVLVTHGATAALAAVV-LATVGPGDRV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 VVPEPAYSLYADLVVLAGGTVDFVPLAPDLHW--DLDALAAALP-GAAMMIFSNPSNPTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 IVHRREELEALGKLLDGTDVLVVSDEAYHRLAYPGHEPVSALEIESLRGRTVYVQTFSKT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 YAMTGWRVGYLT--GPREVLDAAAQVHRTWNGSLNTAVQHAALAALDLPDGVVGAMADRY 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
MEDLINE; 97000351.
REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
RINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map f
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOL. MICROBICL. 21:77-9(1996).
EMBL: AL021411: E1245740; ---
TRANSFERASE; AMINOTRANSFERASE.
SEQUENCE 382 AA; 40860 MW; 9FC8F75A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MIATPPASRIAELRRRSRRPALAPAPPGAVSLAMGEPD-FPTPPTVVQA--AVSA-LREG
                                                                                                                                                                                                                                                     STREPTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPRPGYPNYEARAFNKLEVRHFDLIPDKGWEIDIDSLESIADKNTTAMVIINPNPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 342; DB 2; Length 382;
Pred. No. 1.03e-43;
83; Mismatches 131; Indels 13;
                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
MURPHY L., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                          PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                             292 IVPGWRLGWVAVIDPTKILEKTKISTSITNYLNVST-DPA 330
                                                        235 NCTGWKIGW-A-CGPAELIAGVRAAKQYLSYVGGAPFQPA
                                                                                                                                                  382 AA
                                                                                                                                                  PRT;
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Best Local Similarity 26.1%;
Matches 80; Conservative
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054170
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RESULT

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CETRAINE: 98344137.

KAMARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,

KAMARABAYASI Y., SAWADA M., HORIKAWA H., HOSOYAWA A., NAGAI Y.,

RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,

RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,

RA FUNARAHI Y., TAÑNAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,

RA KIKUCHI H.;

RI "Complete Sequence and Gene Organization of the Genome of a

RI "Complete Sequence and Gene Organization of the Genome of a

RI "Apoloo03; D1030806; -.

RE BABL; APO00003; D1030806; -.

KW TRANSFERASE; AMINOTRANSFERASE.

SQ SEQUENCE 391 AA; 44565 MW; A549ACDA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 PDFDTPKNIKEAAKRALDEG-WTHYTPNAGIPELREAVVEYYKKFYGIDIEVENVIITAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AYEGTYLAFESLLER-GDEVIIPDPAFVSYAEDAKVAEAK-PVR-IPLREENNFLPDPNE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 LLEKIS-KNTR-MIVINYPNNPTGATLD-KELAKTIADIAEDYNIYILSDEPYEHFIYED 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 APFIPMGVFGHIAPVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSIINYLNVS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 -NVASFVQIAGIEAL-RS-EESWKAVEEMKKEYNERRKIVVKRLKNMPGIKVKEPKGAFY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 TDPATFVQEALPKILENTKADFFKRIIGLLKESSEICYREIKENKYITCPH-K-PEGSMF 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 VFPNIS-G--TGMSSE-KFSEWLLEKARVVVIPGTAFGRMGEGYVRISYATSKEKLIEAM 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 VMVKLNLHLLEEIHDDIDFCCKLAKEESVILCPGSVLG-M-ENWVRIFFACVPSSLQDGL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                               ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AKHYPMIKFAPENTILA-NSFSKTFAMTGWRLGFV-V-APSQVI-K-EM-TKLHAYV-IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.2%; Score 330; DB 1; Length 391; Best Local Similarity 28.4%; Pred. No. 2.75e-41; Matches 103; Conservative 82; Mismatches 148; Indels 30;
                                       01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
391AA LONG HYPOTHETICAL ASPARTATE AMINOTRANSFERASE.
391 AA.
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  PRT;
  PRELIMINARY;
                                                                                                                                             PYROCOCCUS HORIKOSHII
                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 1 13:51:53 1999; MasPar time 22.78 Seconds 810.770 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-026-400-2 (1-461) from US09026400.pep 3223 1 MVHQSNGHGEBAAAAANGKS.....LERVKSFCQRNKKRNSINGC 461 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 49.862; Variance 105.736; scale 0.472

### SUMMARIES

	Description Pred. No.	Evrosine transaminase 2 11e-146	transaminase 3.08e-14	aspC protein 2.11e-65	aspartate am 4.	cal protein 7.	£ 1.	transaminas 6.	-		f 2.	Α.	υ.	5	spartate am 1.	Η.	aminotransf 2.	aminotransf 1.	spartate am	aspartate tr 3	membrane pro 2	transaminas 1	transaminas 1	aminotransf 2.68e-2
Ç.	Desc	tvr	tvr	prol	prol	hypo	asp	asp	asp	hypo	asp	asp	hype	asp	pro	aspa	aspa	asp	proj	pro	prof	aspē	aspe	asps
SOFFICES	ΩI	XNRTY	S10887	H70506	D71003	н65000	A70469	80708	H71909	H64603	G70010	A64300	B70815	A38621	E71125	C69591	A69516	B71718	E71009	C69672	S64923	JC5775	JC4537	G69119
	DB	-	7	7	7	7	7	N	~	N	N	~	7	(1	~	~	7	7	7	7	~	~	7	7
	Length	454	454	429	401	405	394	402	390	390	357	375	397	392	391	393	379	412	389	392	592	383	385	374
or (	Query Match	28.5	28.4	15.4	13.6	12.7	12.5	12.2	11.7	11.6	11.4	11.4	11.2	11.1	10.2	10.2	10.0	9.6	9.3	9.3	6.9	9.5	9.5	9.1
	Score	920	914	495	439	410	403	394	376	374	368	368	361	358	330	330	323	308	299	299	300	296	295	294
	Result No.	Н	7	m	4	ഗ	٥	7	Φ.	σ	10	11	12	13	14	12	16	17	18	13	20	21	22	23

probable membrane pro 2.68e-29 aspartate aminotransf 1.30e-28 aminotransferase (Asp 2.15e-26 alanine transaminase (Asp 7.17e-25 aspartate aminotransf 4.98e-24 knurenine aminotransf 4.98e-24 knurenine aminotransf 7.41e-23 aspartate aminotransf 7.39e-22 probable aspartate tr 1.56e-20 aspartate transaminas 2.20e-19 alaninocyclopropane-1 4.42e-18 1-aminocyclopropane-1 9.33e-18 aminotransferase path aminotransferase path aminotransferase path approbable aminotransferase path aminotran	lete (EC 2.6.1.5) - rat rase orvegicus #common_name Norway rat orvegicus #common_name 3: A48430; S18308; S17849 .; Dietrich, J.B.; Chasserot, S.; (N.; Jami, J.; Beck, G.; Pictet, R. 194:347-350 y DNA of rat tyrosine aminotransferase ction of the primary structure of the	GRA GRA GURD:957327; PID:957328 equence was confirmed by protein ble, H.A.; Mathews, W.R.; Baumstark, B.R.; 9) 264:45-53 rosine aminotransferase. Evidence for in catalysis and enzyme turnover. 6-358,'DL',361-444,'D',446-454 ##label HAR anslated the codon GGG for residue 285 as equence was confirmed by protein va, V.S.; Morozov, I.V.; Tishkav, V.I.; 17:994-90. of an ECORI-fragment of the rat tyrosine gene determined on the automated sequencer ms" model 370A.
F65667 PER PART PER	Comp Lnase Lnase Lnase Lnase Lnase Lance JNO34 JNO34 Sefort Sefort Deduce	8
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#journal Eur. J. Biochem. (1991) 201:399-407
#title Expression of mammalian tyrosine aminotransferase in Saccharomyces cerevisiae and Escherichia coli. Purification to homogeneity and characterization of the enzyme overproduced in the bacteria.
#cross-references MUID:92037592
                                                                                                                                                                                                                                                                                                                                                                           Isolation and characterization of active N-terminal truncated app. and holoenzyme of mammalian liver tyrosine aminotransferase.
                                                                                                                  Nucleotide sequence of rat liver tyrosine aminotransferase
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#blnding_site pyridoxal phosphate (Lys) (covalent)
#status experimental
#length 454  #molecular-weight 50635  #checksum 7044
                                                                                                                                                                                                                                                                                    sequence extracted from NCBI backbone (NCBIN:89708, NCBIP:89709)
                                                         S.M.; Popova, V.S.
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acetylated amino end; aminotransferase; homodimer;
phosphoprotein; pyridoxal phosphate
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##residues 190-284,'L',286-386 ##label MOR
##erross-references GB:X15690; NID:957845; PID:91334238
##experimental_source_liver
##residues 385-454 ##label ZEL
##experimental_source liver
RM48430
Athors Advacov, I.V.; Mishin, V.P.; Zelenin,
Mertvetsov, N.P.
Mertvetsov, N.P.
Mertvetsov, Seg. (1990) 1:151-155
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#accession $18308
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##molecule_type protein
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##cross-references GDB:120398; OMIM:276600
#map_position 16q22.1-16q22.3
#introns 79/1; 114/1; 136/3; 189/3; 236/1; 253/3; 304/3; 347/3; 375/3;
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##residues 1-454 ##label RET
##cross-references EMBL:X52509; NID:g36696; PID:e225804; PID:g1217965
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Biochim. Biophys. Acta (1995) 1260:97-101
Cloning and expression of human tyrosine aminotransferase
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                                                                                                                                                      355 LLKESSEICYREIKENKYITCPHKPEGSMFVMVKLNLHLLEEIHDDIDFCCKLAKEESVI 414
286 GWRLGWILIHDRRDIFGN-EIRDGLVKLSQRILGPCTIVQGALKSILQRIPQEFYHDTLS 344
                                                           295 GWRLGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKADFFKRIIG 354
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04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
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Isolation and characterization of the human tyrosine
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##residues 1-454 ##label SER
##cross-references EMBL:X55675; NID:g37501; PID:g37502
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tyrosine transaminase (EC 2.6.1.5) - human
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Bioorg. Khim. (1994) 20:196-204
Nucleotide sequence of human tyrosine
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#cross-references MUID:90326506
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#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
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probable aspC protein - Mycobacterium tuberculosis (strain H37RV)
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##cross-references GB:297991; GB:AL123456; NID:93261837; PID:e330321;
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
109 YAPSIGFLSSREEIASYY-HCPEAPLEAKDVILTSGCSQAIDLCLAVLAN-PGQNILVPR
                                                                  227 KRHLQKILAVAARQCVPILADE1YGDMVFSDCKYEPLATLSTDVPILSCGGLAKRWLVPG
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#length 429 #molecular-weight 47350 #checksum 8456
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Pred. No. 2.11e-65;
86; Mismatches 155; Indels 15;
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Best Local Similarity 29.5%;
Matches 107; Conservative
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##residues 1.401 ##18401 ##1840
##cross-references GB.AP000006; NID:93236133; PID:d1031371; PID:93257745
##experimental_source strain or3
##note this accession replaces an interim accession for a sequence replaced by GenBank
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hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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                                                                                                                                     LWTASTSLAGGTPVHY - LCDETQGWQPDIADLESKITER-TKALVVINPNNPTGAVYSCE
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Pred. No. 4.22e-55;
83; Mismatches 135; Indels 13;
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GB:AD000318; GB:U00096; NID:g1788623; PID:g1788627; ##cross-references GB:AD000318; GB:U00096; NID:g1788627;
                                                                                                                                                                                                      - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYEQRNRAWELINDIPGVSCV-KPRGALYMFPKIDAKRFN-IHDDQKMVLDFLLQEKVLL 363
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LAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMGVEGHIAPVLSIGSLSKSWIVPGWRL 298
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 17 IRGPVLKEAKRLEEEGNK-VLKLNIGNPAPF-GFDAPDEILVDVIRNLPTAQ-G-YCDSK 72
                                                                                                                                                                         hypothetical protein b2290 - Escherichia coli (strain K-hypothetical protein b2290 - Escherichia coli 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 14.Nov-1997
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                                                                                                                                                                                                                                                                                                                                                           #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references_MUID:97426617
                                             SEVREAIDKLARIRICPNTPGQFA--AIAG-LTGSM-DYLKEYMKKLKERRDFIYKRLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.7%; Score 410; DB 2; Length 405;
larity 27.3%; Pred. No. 7.94e-50;
Conservative 94; Mismatches 154; Indels 18;
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Y # #experimental_source_strain_K-12, substrain_MG1655 #C
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                                                                                                      318 IPGIS-TTKPQGAFYIFPRIE 337
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Cubellis, M.V.; Rozzo, C.; Nitti, G.; Arnone, M.I.; Marino, G.; Sannia, G.
Bur. J Blochem. (1989) 186:375-381
Cloning and sequencing of the gene coding for aspartate aminotransferase from the thermoacidophilic archaebacterium
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aspartate transaminase (EC 2.6.1.1) - Sulfolobus solfataricus
aspartate aminotransferase
#formal_name Sulfolobus solfataricus
29-Jan-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-394 ##label AQF ##cross-references GB:AE000766; NID:g2984216; PID:g2984217; GB:AE000657 ##experimental_source strain VF5
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Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.C.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
aspartate aminotransferase - Aquifex aeolicus
#formal_name Aquifex aeolicus
08-May-1998_#sequence_revision 08-May-1998 #text_change
                                                                                                                                                                                                                                                                          #title The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
#cross-references MUID:98196666
#accession A70469
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#superfamily aspartate transaminase
#length 394 #molecular-weight 43777 #checksum 8792
                                                                                                                                                                                                                                                                                                                                                                                               acid sequence not shown;
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Pred. No. 1.47e-48;
87; Mismatches 145; Indels
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#formal_name Helicobacter pylori
strain J99
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Nepsilon-methyllysines by mass spectrometry.
#cross-references MUID:94298815
                                                                                                                                                                                                                                                                                               Zappacosta, F.; Sannia, G.; Savoy, L.A.; Marino,
P.
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                                                                                                                                                                                                                    ##molecule_type protein
##residues 2-38;297-306;308-327;400-402 ##label CU2
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                                                                                                                             ##residues _ 1-402 ##label CUB
##cross-references EMBL:X16505; NID:g47497; PID:g809765
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LGMEN-WVRITFACVPSSLQDGLERVKSF 448
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Sulfolobus solfataricus.
#cross-references MUID:90092126
#accession S07088
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Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Eleischmann, R.D.; Ketchum, K.A.; Klenk,
B.D.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
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The complete genome sequence of the gastric pathogen
Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                             GB:AE001439; NID:94155161; PID:94155168
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Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.
#journal Nature (1999) 397:176-180
#fitle Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter Pylori.
#cross_references_MUID:99120557
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hypothetical protein HP0672 - Helicobacter pylori (strain
26695)
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30-Jan-1998 #sequence_revision 30-Jan-1998 #text_change
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#length 390 #molecular-weight 42746 #checksum 4845
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                                                                                                                                                                                                                                                                                                   ##residues 1-390 ##label ARN ##cross-references GB:AE001493; GE##experimental_source strain J99
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Best Local Similarity 27.3%;
Matches 99; Conservative
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#formal_name Bacillus subtilis
05-Dec-1997 #text_change
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                                                                                                               ##residues 1390 ##label TOM ##residues references GB:AE000511; TIGR:HP0672 CLASSIFICATION #superfamily aspartate transaminase SUMMARY #length 390 #molecular-weight 42874 #checksum 4436
                                           preliminary; nucleic acid sequence not shown;
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Pred. No. 2.40e-43;
85; Mismatches 158; Indels 23;
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#cross-references MUID:97394467
#accession H64603
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                                                                                                ##molecule_type DNA
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Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, Bult, C.J.; White, O.; Olsen, G.J.; EtrzGerald, L.M.; Clayton, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.D.; Cotyne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Xirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glock, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klerk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073 Complete genome sequence of the methanogenic archaeon,
A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, T.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Scklquchi, J.; Sckowska, A.; Serror, R.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, M.; Tanamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognonier, F.; Vassarotti, A.; Viari, A.; Wandler, E.; Wedler, E.; Wedler, H.; Weltzenegger, T.; Winter, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.; Danchin, A. Nature (1997) 390:249-256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 DFEAAVTEKTKAILICSPSNPTGSVYSKEELNEIAEFAKKHDVIVLADEIYAELTYDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *superfamily aspartate transaminase
#length 357 #molecular-weight 39461 #checksum 3672
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aspartate transaminase (EC 2.6.1.1) - Methanococcus
jannaschii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aspartate aminotransferase
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Best Local Similarity 29.8%;
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GB:AL022004; GB:AL123456; NID:g3261550; PID:e1254000;
PID:g2916917
                                                                                                                                                                                                                                                                                                                               16;
                                                                                                       ##recidues 1-375 ##label BUL
##cross-references GB:U67459; GB:L77117; NID:g1590815; PID:g1592252;
TIGR:MJ0001; PID:g1510187
                                                                                                                                                                                                                                                                                                                                                                                                                                   92 ASEALMLSIMTLIDR-GDEVLIPNPSFVSYFSLTEFAEGKIKNIDL--DENFNIDLEKVK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSL- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B70815 #type complete
hypothetical protein Rv0858c - Mycobacterium tuberculosis
(strain H37RV)
#formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                               92 PAFRIAVEAEDAVAAALRIGGFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLIAG 151
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                                                                                                                                                                                                                                                                                                                                                         33 PDFDTPKHIIEAAKRALDEGKTH-YSPNNGIPELREEISNKLKDDYNLDVDKDNIIVTCG 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ESIT-KKTKLIIFNSPSNPTGKVYDKETIKGLAEIAEDYNLIIVSDEVYDKIIYDKKHYS
                                                                                                                                                                                                        #superfamily aspartate transaminase
aminotransferase
#length 375 #molecular-weight 42395 #checksum 1390
                                                                                                                                                                                                                                                                                  Score 368; DB 2; Length 375;
Pred. No. 2.83e-42;
84; Mismatches 117; Indels 18;
                                                           sequence not shown;
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translation not shown
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Methanococcus januaschii.
#cross-references MUID:96337999
#accession A64300
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                                                                                                                                                                                                                                                                                    Query Match 11.4%;
Best Local Similarity 26.3%;
Matches 78; Conservative
                                                                                                                                                                                      #map_position REV3343-2216
CLASSIFICATION #superfamily
                                                                                           ##molecule_type DNA
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A70500
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                                                                                                                                                                                                                                                                             57 YPPGPGSAPLRRAIAAQRRRHFGVDYD-PETEVLVTVGATEAIAAAVLGLVE-PGSEVLL 114
                                                                                                                                                                                           116 YAAGVGLPAARSAVA-EHLSQ-GVPYKLSADDVFLTAGGTQAIEVIIPVLAQTAGANILL 173
                                                                                                                                                                                                                                             115 IEPFYDSYSPVVAMAGAHRVTVPLVPDGRGFALDADALRRAVTPRTRALIINSPHNPTGA 174
                                                                                                                                                                                                                                                                                                                                                                            233 VYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPFIPMGVFGHIA-PVLSIGSLSKSW 291
                                                                                                                                                                                                                                                                                                                                               175 VLSATELAAIAEIAVAANLVVITDEVYEHLVFDHARHLPLAGFDGMAERTITISSAAKMF 234
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23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 13-Sep-1998
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Kagamiyama, H.; Hirotsu, K.; Okamoto, A.; Higuchi,
*length 397 *molecular-weight 42209 *checksum 1391
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11.1%; Score 358; DB 2; Length 392;
Best Local Similarity 23.5%; Pred. No. 1.71e-40;
Matches 85; Conservative 105; Mismatches 154; Indels 18;
                                                    Length 397;
                                                                                                    Indels
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#journal J. Biol. Chem. (1991) 266:2567-2572
#title Thermostable aspartate aminotransferase fro
Bacillus species. Gene cloning, sequence
preliminary X.ray characterization.
#cross-references MUID:91115885
                                               Score 361; DB 2; Le
Pred. No. 5.00e-41;
56; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 NCTGWKIGW-A-CGPAELIAGVRAAKQYLSYVGGAPFQPA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 IVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVST-DPA 330
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Similarity 30.9%;
68; Conservative
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                                               Query Match
Best Local Similarity
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#authors
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 443
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ORGANISM
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                                                                                                                                                                                                                                                                                                                   Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosuqi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Oursuka, R.;
Nakazawa, H.; Takamiya, M.; Offuku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                              probable aspartate aminotransferase - Pyrococcus horikoshii #formal_name Pyrococcus horikoshii 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFPNIS-G--TGMSSE-KFSEWLLEKARVVVIPGTAFGRMGEGYVRISYATSKEKLIEAM 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 PDFDTPKNIKEAAKRALDEG-WTHYTPNAGIPELREAVVEYYKKFYGIDIEVENVIITAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NVASFVQIAGIEAL-RS-EESWKAVEEMKKEYNERRKIVVKRLKNMPGIKVKEPKGAFY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 PAFRIAVEAEDAVAAALRIGOFNCYAAGVGLPAARSAVAEHLSOGVPYKLSADDVFLIAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AYEGTYLAFESLLER-GDEVIIPDPAFVSYAEDAKVAEAK-PVR-IPLREENNFLPDPNE 157
                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AKHYPMIKFAPENTILA-NSFSKTFAMTGWRLGFV-V-APSQVI-K-EM-TKLHAYV-IG
                    329 DVSEAAQKTGFASVDEFASALLTEANVAVIPGSGFGAPSTIRISYATSLNLIEEAIERID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 391 #molecular-weight 44565 #checksum 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 330; DB 2; Length 391;
Pred. No. 1.50e-35;
82; Mismatches 148; Indels 30;
                                                                                                                                                                                                     #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
##residues 1-391 ##label KAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.2%;
Best Local Similarity 28.4%;
Matches 103; Conservative
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                                                                                                                                SF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #residues
                                                                                             389 RF 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##status
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REFERENCE
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ORGANISM
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Aubst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bololin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Desterhoeft, A.;
Ebriet, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Eujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandl,
G.; Guy, B.J.; Haga, K.; Hałech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Ttaya, M.; Jones, L.; Joris, B.; Karamata,
D.; Kasahara, Y.; Kaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krappel, S.; Hasmoto,
M.; Moestl, D.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Doll, T.M.; Portectale, D.; Porvolik, S.; Prescort,
V.; Medigue, C.; Medina, N.; Mellado, R.P.; Parro,
V.; Pobl, T.M.; Portectale, D.; Porvolik, S.; Prescort,
V.; Pobl, T.M.; Portectale, D.; Porvolik, S.; Soldo,
B.; Sorokin, A.; Seror, S.J.; Scrifone, F.; Sektyuchi, J.;
Sekowska, A.; Seror, S.J.; Scrifone, F.; Sektyuchi, J.;
Tarkemaru, K.; Taeconi, E.; Pujic, P.; Purnelle, B.; Rabmato,
Takemaru, K.; Taeconi, E.; Padaie, Y.; San,
Tarkemaru, K.; Taeconi, E.; Wedler, H.; Weitzenegger, T.;
Tarkemaru, K.; Taeconi, E.; Wedler, H.; Weitzenegger, T.;
Tarkemaru, K.; Taeconi, E.; Wedler, H.; Weitzenegger, T.;
Tarkemaru, R.; Voshikaw, H.; Danchin, A.; Tamamoto, H.F.; Zumstein, E.;
Walters, P.; Wippt, A.; Yananamoto, H.F.; Zumstein, E.;
Walters, P.; Willer, W.; Vara, Yana, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                    #formal_name Bacillus subtilis
05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #superfamily aspartate transaminase
#length 393 #molecular-weight 43088 #checksum 6856
                                  aspartate aminotransferase aspB - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 10.2%; Score 330; DB 2; Length 393; Local Similarity 23.2%; Pred. No. 1.50e-35; S5; Conservative 117; Mismatches 145; Indels 20;
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#type complete
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##experimental_source strain 168
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Oct 1 13:50:18 1999; MasPar time 15.42 Seconds 844.953 Million cell updates/sec Tabular output not generated. Run on:

Title:

>US-09-026-400-2 (1-461) from USO9026400.pep 3223 1 MVHQSNGHGBAAAAANGKS.....LERVKSFCQRNKKNSINGC 461 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 51.018; Variance 91.346; scale 0.559 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		dР			SUMMAKIES		
Result No.	Score	Query Match	Lengt	DB	Ü	Description	Pred. No.
н	920	28.5	454	-	ATTY RAT	TYROSTNE AMMOTRANCE	3 400-173
7	914	28.4	454	-	ATTV UITMAN		0.1.0
(*)	570	17.7	416	1	CONCE VERY	TANDOLINE AMINOIRANSFER	8.32e-1/2
,	0 0		7	٠,	ATTITUE	TIKOSINE AMINOIKANSFEK	5.466-94
<b>4</b> , 1	47.0	77.7	40T	-	AAT_SULSO	ASPARTATE AMINOTRANSFE	1.09e-55
Ω,	368	11.4	375	Н	AAT1_METJA	PUTATIVE ASPARTATE AMI	3.41e-50
٥	358	11.1	392	Н	AAT_BACSP	ASPARTATE AMINOTRANSFE	4.286-48
7	345	10.7	393	П	AAT_BACST	ASPARTATE AMINOTRANSFE	2.226-45
ω .	330	10.2	393	Н	AAT1_BACSU	ASPARTATE AMINOTRANSFE	2.86e-42
o i	301	ص	392	Н	PATA_BACSU	PUTATIVE AMINOTRANSFER	2.51e-36
10	300	9.3	592	<del>(  </del>	ALAM_YEAST	PUTATIVE ALANINE AMINO	00e-3
11	294	9.1	207	Н	ALAT_YEAST	PUTATIVE ALANINE AMINO	6.58e-35
12	285	8.	400	Н	AATA_RHIME	ASPARTATE AMINOTRANSFE	4.29e-33
13	258	8.0	444	Н	YJG0_YEAST	HYPOTHETICAL AMINOTRAN	1.01e-27
14	255	7.9	505	Н	ALAT_SCHPO	PUTATIVE ALANINE AMINO	3.91e-27
15	241	7.5	410	Н	AATB_RHIME	ASPARTATE AMINOTRANSFE	2.09e-24
16	243	7.5	421	М	YDT4_SCHPO	HYPOTHETICAL AMINOTRAN	8.56e-25
17	235	7.3	386	m	YBDL_ECOLI	HYPOTHETICAL AMINOTRAN	3.00e-23
18	231	7.2	482	근	ALA2_HORVU	ALANINE AMINOTRANSFERA	1.75e-22
19	222	6.9	387	н	PATB_BACSU	PUTATIVE AMINOTRANSFER	9.06e-21
20	221	6.9	399	Н	AAT2_BACSU		1.400-20
21	222	6.9	517	Н	1A1C DIACA	1-AMINOCYCLOPROPANE-1-	9 066-21
22	217	6.7	482	Н	ALA2 PANMI	ALANINE AMINOTRANSFERA	7.966-20
23	211	6.5	213	H	AAT_STRGR	PROBABLE ASPARTATE AMI	

e-1	9-1	.88e-1		1 - 0	.64e-1	02e-1	02	58e-1	37e-1	64e-1	.29e-1	.92e-1	85e-1	.22e-1	•	H	36	966-0	.42e-0	.41e-0	
HISTIDINOL-PHOSPHATE A	PUTATIVE AMINOTRANSFER	Æ,	I-AMINOCICLOPROPANE-I- HISTIDINOI-PHOSPHATE A	$\alpha$	H		ч	1-AMINOCYCLOPROPANE-1-	ALANINE AMINOTRANSFERA	MALY PROTEIN (EC 2.6.1	1-AMINOCYCLOPROPANE-1-	PUTATIVE ASPARTATE AMI	1-AMINOCYCLOPROPANE-1-	1-AMINOCYCLOPROPANE-1-	HISTIDINOL-PHOSPHATE A	HISTIDINOL-PHOSPHATE A	PUTATIVE AMINOTRANSFER		HISTIDINOL-PHOSPHATE A	Δ.	
HIS8_YEAST	- 1	YFDZ_ECOLI	HISS HALVO		YJIR_ECOLI	HIS8_SULSO	1A11_CUCMA	1A11_CUCPE	ALAT_HUMAN	MALY_ECOLI	1A12_CUCPE	AAT2_METJA	1A1C_MALDO	1A14_LYCES	HIS8_MYCSM	HIS8_SCHPO	YU16_MYCTU	YB66_HAEIN	HIS8_SALTY	HIS8_METJA	
П	Α,	٦,		Н	Н	Н	Н	н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	
385	418	414	361	495	470	376	493	493	495	390	464	370	473	476	219	384	407	366	359	373	
6.5	 	•		6.1	•	•				•				5.1						4.8	
211	210	700	195	195	187	185	179	177	176	170	166	165	164	163	160	162	160	158	155	156	
24	52	0 6	7 7 8 7 8	53	30	31	32	33	34	35	36	37	80 ·	ტ წ	40	41	42	43	44	45	

## ALIGNMENTS

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HOMO
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.49e-173;
117; Mismatches 135; Indels 11; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWRLGWILIHDRRDIFGN-EIRDGLVKLSQRILGPCTIVQGALKSILQRTPQEFYHDTLS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 LLKESSEICYREIKENKYITCPHKPEGSMFVMVKLNLHLLEEIHDDIDFCCKLAKEESVI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 SNKTFNPIRAIVDNMKVQPNPNKTVISLSIGDPTVFGNLPTDPEVTQAMKDALDSGKYNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 AKNSIRAIRYKISA-SVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRTGQFNC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAPSIGYLSSREEVASYYHCHEAP--LEAKDVILTSGCSQAIELCLAVLAN-PGQNILIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPGFSLYRTLAESMGIEVKLYNLLPEKSWEIDLKQLESLIDEKTACLVVNNPSNPCGSVF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKRHLQKILAVAERQCVPILADEIYGDMVFSDCKYEPLANLSTNVPILSCGGLAKRWLVP 285
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                                                                                                                                      -:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- PATHWAY: FIRST STEP IN THE CATABOLISM OF TYROSINE.
-:- SUBUNIT: HOMODIMER.
-:- TISSUE SPECIFICITY: LIVER.
-:- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00155; aminotran_1; 1.
TYROSINE CATABOLISM; TRANSFERASE; AMINOTRANSFERASE; ACETYLATION;
and immunochemical properties of rat liver tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE.

IV -> KT (IN REF. 2).

TA -> LE (IN REF. 3).

MISSING (IN REF. 3).

AI -> DL (IN REF. 3).

A -> DL (IN REF. 2).

A -> D (IN REF. 2).

A -> D (IN REF. 2).
                                                                                        2-OXOGLUTARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 LC-PGSVLGMENWVRITFACVPSSLQ-DGLERVKSFCQRN 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                       BIOCHIMIE 70:673-679(1988).
-!- CATALYTIC ACTIVITY: L-TYROSINE + 2-OXC 4-HYDROXYPHENYLPYRUVATE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00105; AA_TRANSFER_CLASS_1; 1.
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Matches 137; Conservative
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454 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE, 93028451.
MATT E., KIDA K., ODIEVRE M., DI ROCCO M., SCHERER G.;
"Point mutations in the tyrosine aminotransferase gene in tyrosinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- CATALTIC ACTIVITY: L-TYOSINE + 2-0XOGLUTARATE = 4-HYDROXYPHENYLPYRUVATE + 1-CLUTAWATE.
-:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- PATHWAY: FIRSY STEP IN THE CATABOLISM OF TYROSINE.
-:- SUBMINT: HOMODIMER.
-:- TISSUE SPECIFICITY: LIVER.
-:- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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BINDING 280 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

BINDING 280 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

ARRIANT 362 362 G -> V (IN TYROSINEMIA, TYPE II).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95092801.
SEALINI G.E., LUU-THE V., LABRIE F.;
"Cloning and expression of human tyrosine aminotransferase CDNA.";
BIOCHIM. BIOPHYS. ACTA 1260:97-101(1995).
                01-AUG-1990 (REL. 15, CREATED)
1-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST AND TATION UPDATE)
TYROSINE AMINOFRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE
                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                            MEDLINE; 90326506.

RETTENMEIER R., NATT E., ZENTGRAF H., SCHERER G.;
"Isolation and characterization of the human tyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type II.";
PROC. NAIL, ACAD. SCI. U.S.A. 89:9297-9301(1992)
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EMBL, X2510; E22504; JOINED.
EMBL, X2511; E225804; JOINED.
EMBL, X2511; E225804; JOINED.
EMBL, X52513; E225804; JOINED.
EMBL, X52513; E225804; JOINED.
EMBL, X52514; E225804; JOINED.
EMBL, X52516; E225804; JOINED.
EMBL, X52516; E225804; JOINED.
EMBL, X52518; E225804; JOINED.
EMBL, X52519; E225804; JOINED.
EMBL, X55519; E225804; JOINED.
EMBL, X5550; G36713; --
EMBL, X55675; G37502; --
PIN; S10887; S10887.
MIM; 276600; --
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                       NUCLEIC ACIDS RES. 18:3853-3861(1990).
                                                                                              AMINOTRANSFERASE) (TAT).
                                                                                                                                SAPIENS (HUMAN).
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SEQUENCE FROM N.A.
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                                                                                                                                                                49 AKKIFNPIRAIVDNMKVKPNPNKTMISLSIGDPTVFGNLPTDPEVTQAMKDALDSGKYNG 108
                                                                                                                                                                                                                                                  57 AKNSIRAIRYKISA-SVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRIGQFNC 115
                                                                                                                                                                                                                                                                                                                                         YAPSIGFLSSREEIASYY-HCPEAPLEAKDVILTSGCSQAIDLCLAVLAN-PGQNILVPR 166
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4-HYDROXYPHENYLPRUVATE + L-GLUTAMATE.
A AROMATIC OXO ACID + L-GLUTAMATE.
COFACTOR: PYRIDOXAL PHOSPHATE.
PATHWAY: FIRST STEP IN THE CATABOLISM OF TYROSINE.
SUBUNIT: HOWODIMER.
SUBCLILOLAR LOCATION: MAINLY CYTOSOLIC. PRESENT TO A SWALL EXTENT IN THE MITOCHONDRIAL FRACTION.
PTM: THREE DISULFIDE BONDS ARE PRESENT.
PTM: THREE DISULFIDE BONDS ARE PRESENT.
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EUKARYOIA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
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"Purification and partial structural and kinetic characterization of tyrosine aminotransferase from epimastigotes of Trypanosoma cruzi.";
BIOCHEM. J. 292:901-906(1993).
-!- FUNCTION: COULD TRANSAMINATE TRYPTOPHAN, PHENYLALANINE AS WELL
AS TYROSINE. THIS PARTICULAR ENZYME MAY ALSO BE AN ALANINE
                                                                                                Gaps
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12. LAST SEQUENCE UPDATE)
12. LAST ANNOTATION UPDATE)
13. LAST ANNOTATION UPDATE)
14. TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE
15. AMINOTRANSFERASE) (TATA)
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SEQUENCE OF 120-148; 153-167 AND 324-338, AND CHARACTERIZATION
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MEDLINE: 93341574.
BONTEMPI E.U., BUA J., ASLUND L., PORCEL B., HENRIKSSON J.,
BONTEMPI E.U., BUA J., ASLUND L., PORCEL B., HENRIKSSON J.,
ISOLATION and characterization of a gene from Trypanosoma c
encoding a 46-kilodalton protein with homology to human and
tyrosine aminotransferase.";
         DB 1; Length 454;
                                                                                           Indels
    Score 914; DB 1; Le
Pred. No. 8.32e-172;
119; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUBELLIS M.V., ROZZO C., NITTI G., ARNONE M.I., MARINO G., SANNIA G., "Cloning and sequencing of the gene coding for aspartate aminotransferase from the thermoacidophilic archaebacterium
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            16
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                         18 PIR-TVSDNAKPSPSPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDSQECNGYFPTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPEAREAVATWWRNSFVHKEELKSTIVKDNVVLCSGGSHGILMAITAICD-AGDYALVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGFPHYETVCKAYG-IGMHFYNCRPENDWEADLDEIRRLKDDKTKLLIVTNPSNPCGSNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 SRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPRVILGGTAKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 LVVPGWRLGWL-LYVDPHGNGPSFLEGLKRVGML-VC-GPCTVVQAALGEALLNTPQEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 WIVPGWRLGWVAVY-DPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKADFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 DQIVAKIEESAMYLYNHIGECIGLA-PIMPRGAMYLMSRIDLEKYRDIKIDVEFFEKLLE
                                                                                                                                                                                                                                                             PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT). SULFOLOBUS SOLFATARICUS.
ARCHAEA; CRENARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                             Length 416;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 EENVQVL-PGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRH 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-38 AND 296-326.
STRAIN-ATCC 49255 / MT4;
MEDLINE; 90092126.
                                                                                                                                                                                      PROSITE; PS00105; AA_TRANSPER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TYROSINE CATABOLISM; TRANSPERASE; AMINOTRANSFERASE;
PYRIDOXAL PHOSPHATE (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:| :| ||:::||:||||||EESV-ILCPGSVLGMENWVRITFACVPSSLQDGLERVKSFCQRN
                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.46e-94;
105; Mismatches 152;
                                                                                                                                                                                                                                                                                                                        17.7%; Score 570; DB 1; 30.9%; Pred. No. 5.46e-94;
                                                                                                                                                                                                                                                                           153 H -> D (IN REF. 2
46167 MW; AC035E2B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT_SULSO STANDARD; PRT; 401 AA. P14909; 01-APR-1990 (REL. 14, CREATED) 01-APR-1990 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                         EMBL; L00673; G408894; --
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUR. J. BIOCHEM. 186:375-381(1989)
                                                                                                                                                                                                                                                                                                                                                          Conservative
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SEQUENCE, AND METHYLATION.
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                                                                                                                                                                                                                                                                       153 1
416 AA;
                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 125; Conser
                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AEVARKLGILVIADEVYGKLVLGSAPFIPMGVFGHIAPVLSIGSLSKSWIVPGWRLGWVA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 ARSAVAEHLSQGVPYKLSADDVFLTAGGTQAIEVIIPVLAQTAGANILLPRPGYPNY-EA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDISRDNKIILLSDEIYDNFVYEGKMRSTLEDSDWRDFLIYVNGFSKTFSMTGWRLGYI- 253
                       ZAPPACOSTA F., SANNIA G., SAVOY L.-A., MARINO G., PUCCI P.; "Post-translational modifications in aspartate aminotransferase from Sulfolobus solfataricus. Detection of N-epsilon-methyllysines by mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 YK-ISASVEESGPRPVLPLAHGDPSVFPAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 LREKIAQYLNTRYGTDVKKEEVIVTPGAKPALFLVF-ILYINPSDEVILPDPSFYSYAEV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 VKLLGGKPIYANLKWSREEGFSIDVDDLQSKISKRTKMIVFNNPHNPTGTLFSPNDVKKI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 YKEIARNVEKTKKIKIIDFGIGQPDL-PTFKR-IR--DAAKEALDQG-FTFYTSAFGIDE 75
                                                                                                                                                                                                                                                                                 -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBGNIT: HOMODIMER.
-!- THIS ENZIME OPTIMUM TEMPERATURE IS ABOVE 95 DEGREES CELSIUS.
-!- THIS ENZIME OPTIMUM CEMPERATURE IS ABOVE 95 DEGREES CELSIUS.
-!- SIMILARIYE: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                      DE ROSA M.; "Purification and characterization of aspartate aminotransferase the thermoacidophilic archaebacterium Sulfolobus solfataricus."; J. BIOL. CHEM. 263:12309(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE; METHYLATION
                                                                                                                                                                                                                                                          G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRIDOXAL PHOSPHATE.
METHYLATION (MONO-) (PARTIAL).
METHYLATION (MONO-) (PARTIAL).
DF51D490 CRC32;
                                                                                                                                                                                                             SEGUENCE OF 239-250.
STRAIN-ATCC 49255 / MT4;
BIDLINE; 92062095.
BIROLO. ARNONE M.I., CUBELLIS M.V., ANDREOTTI G., NITTI MARINO G., SANNIA G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
12.2%; Score 394; DB 1; Length 401;
Best Local Similarity 24.7%; Pred. No. 1.09e-55;
Matches 96; Conservative 118; Mismatches 153; Indels 3
                                                                                                  SEQUENCE OF 1-22.
STRAIN-ATCC 49255 / MT4;
MEDLINE; 88315018.
MARINO G., NITTI G., ARNONE M.I., SANNIA G., GAMBACORTA
                                                               spectrometry.";
EUR. J. BIOCHEM. 222:761-767(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 M
45600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X16505; G809765; -.
STRAIN-ATCC 49255 / MT4; MEDLINE; 94298815.
                                                                                                                                                                                                                                                                                                                                                                                                    AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S07088; S07088.
S18362; S18362.
S21189; S21189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
202
384
401 AA;
                                                                                                                                                                                                                                                                                                                                         L-GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
SEQUENCE
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PROSITE;
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PIR;
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Pred. No. 3.41e-50;
84; Mismatches 117; Indels 18; Gaps 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANE J.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANE J.D.,
KERLAYAGE A.R., DOUGHERTY B.A., TONB J.F., ADAMS M.D., RELOR C.I.,
OVERBEEK R., KIRNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.K., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 ASEALMLSIMTLIDR-GDEVLIPNPSFVSYFSLTEFAEGKIKNIDL--DENFNIDLEKVK 148 :::|: : | | : | : | : | : : | : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG 151
254 V-AKREIIQK--MGI-LAA--NVYTAPTSFVQKAAVKAFD-TFDEV-NQMVSLFKKRRDV 305
                                              MYDELIKVKGVEVS-KPNGAFYMFPNVSKILKTSGFDVKSLAIKLIEEKGVVTIPGEVFP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: L. ASPARTATE + 2-OXOGLUTARATE - OXALOACETATE L-GLUTAMATE (BY SIMILARITY)
-:- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)
-:- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
42395 MW; 166A9EFC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE ASPARTATE AMINOTRANSFERASE 1 (EC 2.6.1.1) (TRANSAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AA.
                                                                                                                                                                                                                                                                                                                                                    LGMEN-WVRITFACVPSSLQDGLERVKSF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
                                                                                                                                                                                                                                                                                 LNIGKEFLRLSFAVNEEVIKEGIQKIREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCIENCE 273:1058-1073(1996).
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es 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT1_METJA
060317;
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GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSL- 210
                                                       208 PMQ-FTDRC-IL-INGFSKTYAMTGWRIGYLAVSDELNKELDLINNMIKIHQY-SFAC-A 262
                                                                                                                            SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H., HIROTSU K., OKAMOTO A., HIGUCHI T., SODA K.;
"Thermostable aspartate aminotransferase from a thermophilic Bacillus species. Gene cloning, sequence determination, and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification and characterization of thermostable aspartate aminotransferase from a thermophilic Bacillus species.";
J. BACTERIOL. 172:1345-1351(1990).
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THIS THERMOSTABLE ENZYME IS MOST ACTIVE AT 70 DEGREES CELSIUS. SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                         263 TIFAQYGALA-ALRGSQ-KCVEDMVREFKMRRDLIYNGLKDI-FKV--NKPDGAFYI 314
                                                                                                                                                                                                      330 ATFVQ-EALPKILENTKADFFKKIIGLKESSEICYREIKENKYITCPHKPEGSMFV 385
                                     ESIT-KKTKLIIFNSPSNPTGKVYDKETIKGLAEIAEDYNLIIVSDEVYDKIIYDKKHYS
                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
BACILLUS SP. (STRAIN YM-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
                                                                                                                                                                                                                                                                                                                                                                                                         BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 239 239 PYRIDOXAL PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 1; I
4.28e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> L (IN REF. 2
8F0EC6D0 CRC32;
                                                                                                                                                                                                                                                                                      392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A38621; A38621.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 358;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOL. CHEM. 266:2567-2572(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                             AAT_BACSP STANDARD; E P23034; 01-NOV-1991 (REL. 20, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-24 AND 387-392.
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larity 23.5%; F
Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M59430; G142538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 91115885.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-GLUTAMATE.
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PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG 151
                                    AKHVLYTLFQVILN-EGDEVIIPIPYWVSYPEQVKLAG-GVPVYIEATSEQNYKITAEQL 158
                                                                                                          KNAITDK-TKAVIINSPSNPTGMVYTREELEDIAKIALENNILIVSDEIYEKLLYNGAEH 217
                                                                                                                            QYAA-I-EAY-NGPQDSVEEMRKAFESRL-ET--I-YPKLSAIPGFKVV-KPQGAFYLLP 328
                                                                                                                                                                                                                                                                           -1- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
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                                                                                                                                                                                                                                                                                                                            329 DVSEAAQKTGFASVDEFASALLIEANVAVIPGSGFGAPSTIRISYATSLNLIEEAIERID
                                                           GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHF-DLIPDKGWEIDIDSL
                                                                                                                                                                               FSIAQISEEVKAQTIVINGVSKSHSMTGWRIGYAAG-NADIINAMTDLASHSTSNPTTAS
                                                                                                                                                                                                                 FIPMGVFGHI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSTINYLNVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BARTSCH K., SCHNEIDER R., SCHULZ A., Stareospecific production of the herbicide phosphinothricin "Stereospecific production of aspartate transaminase from Bacill stearchermophilus, cloning of the corresponding gene, aspC, and application in a coupled transaminase process."; APPL. ENVIRON. MICROBIOL. 67:3794-3799(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PRAN; PF00155; AA_TRANSFERASE; PYRIDOXAL PHOSPHATE.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 237 237 237 SERUCOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 345; DB 1; Length 393
Larity 23.8%; Pred. No. 2.22e-45;
Conservative 104; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X93600; E212847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMINOTRANSFERASES.
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 12980;
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17;

Gaps

18;

42 PDFNTPQNIMDAAIDSMQQG-YTKYTPSGGLPALKQAIIEKFKRDNQLEYKPNEIIVGVG 100

105; Mismatches 154; Indels 18;

85.

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Query Match
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Matches
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                                                   156
                                                                          210
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                                                                                                                                                  268
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                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                   NAREAAAMAGCRTVDEFVAALLEEAKVALVPGSGFGAPDNVRLSYATSLDALETAVERIH 386
                                                                                                                                                                                                                                                                  388 KL-NLHLLEEIHDDIDFCCKLAKEESVILCPGSVLGMENWVRITFACVPSSLQDGLERVK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the Bacillus subtilis chromosome region between
                          151
  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the serA and kdg loci cloned in a yeast artificial chromosome.";
MICROBIOLOGY 142:2005-2016(1996).
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNTT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L47709; G1146246; -.
EMBL; 209115; E1183682; -.
EMBL; 209115; E1183682; -.
EMBL; 209115; AA_TRANSFER_CLASS_1; 1.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PRAM; PF001155; anihotran_1; 1.
PRAM; PF001155; anihotran_1spring.

237 PARISONAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                    :|:::| | | ||:|:::
DPATFVQEALPKILENTKADFFKRIGLLKESSEICYREIKENKYITCPHKPEGSMFVWV
                                                                    : :|: :: || : | ::::| | : : : : : : | | : | CTQAIEVIIPVLAQTAGANILLLPRPGYPNYEARAAFNKLEVRHF-DLIPDKGWEIDIDSL
                                                                                                                           211 -ESIADKNTTAMVIINPNNPCGSVYSYDHLAKVAEVARKLGILVIADEVYGKLVLGSAPF
                                                                                                                                                    VSIAELSPELKAQTVIINGVSKSHSMTGWRIGYAA - GPKDII - KA - M-TDLASH - STS -
                                                                                                                                                                   270 IPMGVFG-HI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVST
                                                                                                                                                                                                    NPTSIAQYAAIAAYSGPQEPV-EQMRQAFEQRLNIIYDKLVQIPGFTCV-KPQGAFYLFP
  PDFNTPQHILDAAIKAMNEGHTK-YTPSGGLPALKEEIIKKFARDQGLDYEPAEVIVCVG
                          PAFRTAVEAEDAVAAALRTGQFNCYAAGVGLPAARSAVAEHLSQGVPYKLSADDVFLTAG
                                                   AKHALYTLFQVLLD-EGDEVIIPTPYWVSYPEQVKLAG-GVPVYVEGLEQNHFKITPEQL
                                                                                                   KQAITPR-TKAVIINSPSNPTGMIYTAEELKALGEVCLAHGVLIVSDEIYEKLTYGGAKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOROKIN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                393 AA.
                                                                                                                                                                                                                                                                                                                                                                                PRT;
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58 / MARBURG;
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MEDLINE; 96349105.
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P53001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 FIPMGVFG-HI-APVLSIGSLSKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVS 326
                                                                                                                                                              327 IDPATEVQEALPKILENTKADFFKRIIGLLKESSEICYREIKENKYITCPHKPEGSMFVM 386
                                                                                                                                                                                                                                             TGAKHALYTLEQVILD-EEDEVIIPTPYWVSYPEQVKLAGGKPVYVEGLEENHFKISPEQ 155
                                                                                                                                                                                                                                                                                                                                                                  LKNAITEK-TKAIVINSPSNPTGVMYTEEELSALGEVCLEHDILIVSDEIYEKLTYGGKK 214
                                                               Gaps
                                                                                                                        40 PDFNTPQHIIDAAVRSMNEGHTK-YTPSGGLAELKNSIAEKFKRDQNIEYK-PSQ-IIVC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTONIEWSKI C., SAVELLI B., STRAGIER P.; "The spoil gene, which regulates early developmental steps in Bacillus subtilis, belongs to a class of environmentally responsive

    J. BACTERIOL. 172:86-93(1990).
    -1- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
    -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 -NPTSIAQYG-AIAAYNGPSEPLEEMREAFEHRLNTIYAKLIEIPGFSCV-KPEGAFYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNAKEAAQSCGFKDVDEFVKALLEEEKVAIVPGSGFGSPENVRLSYATSLDLLEEAIERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 HVSIAQLSDRLKEQTVIINGVSKSHSMTGWRIGYAA--GSEDII-KA-M-TNLASH-STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACILLUS SUBTILIS.
BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                            20;
Length 393;
10.2%; Score 330; DB 1; Length 393 tarity 23.2%; Pred. No. 2.86e-42; Conservative 117; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCANLAN E., DEVINE K.M.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (REL. 15, CREATED)
15-UUL-1998 (REL. 36, LAST SEDUENCE UPDATE)
1-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PUTATIVE AMINOTRANSFERASE A (EC 2.6.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392
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EMBL; 299111; E1184990; -.
EMBL; M29450; G143632; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                            Local Similarity
es 85; Conserves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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P16524;
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WALSH S.V.;
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P52892;
                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341
              요
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE ALANINE AMINOTRANSERASE, MITOCHONDRIAL PRECURSOR
(EC. 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,

FAVELLO A., FULTON L., GATTING S., GRECO T., KIRSTEN J., KUCABA T.,

HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,

JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,

MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,

TACH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,

WILSON R., WATERSTON R.,

SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                          108 IRTGOFNCYAAGVGLPAARSAVAEHLSOGVPYKLSADDVFLTAGGTQAIEVIIPVLAQTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 GDEVIMPGPIYPGYEPIINLCGAKPVIVD-TTSHGFKLTARLIEDALTPNTKCVVLPYPS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 GANILLPRPGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSLESIADKNTTAMVIINPN 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPTGVTLSEEELKSIAALLKGRNVFVLSDEIYSELTYDRPHY-SIATYLRDQTIV-INGL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKSHSMTGWRIGFL--FAPKDI-AK-HI-LKVHQY-NVSCASSISQKAALEAVTNGLDDA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334
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                                                                                                                                                                                                                                                              1 MEHLLNPKAREIEISGIR-KFSNLVAQHED--VISLTIGQPDFFTPHHVKAAAKKAIDEN 57
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                       58 V-TS-YTP-NAGY-L-ELRQAVQLYMKKKADFNYDAESEIIITTGAQAIDAAFRTIL-SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 SKSWIVPGWRLGWVAVYDPTKILEKTKISTSITNYLNVSTDPATFVQEALPKILENTKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 LIMR--EQYKKRLDYVY-DRLVSMGLDVV-KPSGAFYIFPSIK-SF--GM-TSFDFSMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 FFKRIIGLIKESSEICYREIKENKYIICPHKPEGSMFVMVKLNLHLLEEIHDDIDFCCKL
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                                                                                       SIMILARITY)
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EURARYOTA: FUNGI: ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 LEDAGVALVPGSSFSTYGEGYVRLSFACSMDTLREGLDRLELFVLKKREAMQTIN 389
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                                                                                                                                                                 Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-GLUTAMATE.
-:- COFACTOR: PYRIDOXAL PHOSPHATE.
-:- SUBCELLULAR LOCATION: MITOCHONDRIAL (POTENTIAL).
-:- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
                                                                                                                                                        Score 301; DB 1; Length 392
Pred. No. 2.51e-36;
102; Mismatches 187; Indels
           SUBLIDIAGE, COLONIA ATTRANSFER_CLASS_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 230 230 PYRIDOXAL PHOSPHATE (BY SEQUENCE 392 AA; 43414 MW; 899A4D38 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 AA.
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                                                                                                                                                           Match 9.3%;
Local Similarity 23.4%;
les 97; Conservative 1
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  BG10205;
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TRANSAMINASE)
  SUBTILIST;
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P52893;
                                                                                                                                                              Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 YSSSQGVEGIRKSVAEFITKRDEGEISYPEDIFLTAGASAAVNYLLSIFCRGPETGVLIP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 IPQYPLYTATLALNNSQALPYYLDENSGWSTNPEEIETVVKEAIQNEIKPTVLVVINPGN 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA, FUNGI, ASCOMYCOTA, HEMIASCOMÝCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRIDOXAL PHOSPHATE (BY SIMILARITY). 5FF91EE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRIDOXAL PHOSPHATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTATIVE ALANINE AMINOTRANSFERASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŚEÓUENCE FROM N.A.
STRAIN-S288C / AB972;
MURPHY L., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- CATALTIAN CATIVITY: L-ALANINE + 2-OXOGLUTARATE - PYRUVATE L-GLUTAMATE.
-1- COFACTOR: PYRIDOXAL PHOSPHATE.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-1- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                EMBL; 273261; E245543; -.
EMBL; 273261; E245543; -.
HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
HYPOTHETICAL PROTEIN; TRANSIT PEPTIDE
PYRIDONAL PHOSPHATE; MITOCHONDRION (POTENTIAL).
MITOCHONRION (POTENTIAL).
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01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-00T-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE ALABINE ANINOTRANSFERASE (EC 2.6.1.2) (GLUTTRANSAMINASE) (GPT)_(GLUTAMIC--ALANINE TRANSAMINASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.00e-36;
stches 53;
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50; Mismatches
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YDR111C OR YD9727.07C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 4
592 AA;
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                                                                        SO VLPLAHGDPSVFPAF-RIAVEAEDAVAAALRIGGFNCYAAGVGLPAARSAVAEHLSQ-GV 137
                                                                                                               218
                                                                                                                                            197
                                                                                                                                                                                      100 ILRVGHNELASLNLFSRDALERAERLLNDI-GGSIGAYSHSQGVPGIRQTVADFITRRDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILIE; 93209934.

WATSON R.J., RASTOGI V.K.;

"Cloning and nucleotide sequencing of Rhizobium meliloti
"Cloning and nucleotide sequencing of shizobium meliloti
aminotransferase genes: an aspartate aminotransferase required for symbiotic nitrogen fixation is atypical.";
J. BACTERIOL. 175:1919-1928(1993).
-i. FUNCTION: REQUIRED FOR SYMBIOTIC NITROGEN FIXATION.
-i. CATALITIC ACTIVITY: L.ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RASTOGI V.K., WATSON R.J.;
"Aspartate aminotransferase activity is required for aspartate catabolism and symbiotic nitrogen fixation in Rhizobium meliloti.";
J. BACTERIOL. 173:2879-2887(1991).
                              Gaps
                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (REL. 26, CREATED)
1-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANOTATION UPDATE)
ASPARTATE AMINOTRANSFERASE A (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 GEPATPEDIYLTTGASSAATSLLSLLCKDSQTGLLIPIPQYPLYTASASLFNAQVLPYYL
                                                                                                                                  DEESNWSTNSDEIEKVVQDALKKQIRPSVLIVINPGNPTGAVLSEETIARICLIAAKYGI
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                              6
 Length 507;
                            Indels
Score 294; DB 1;
Pred. No. 6.58e-35;
                              Mismatches
                                                                                                                                                                                                                                                                                                                    400 AA
                                                                                                                                                                                                                                                                                                                     PRT;
                              61;
                                                                                                                                                                                                                                                   252 LVIADEVYGKLVLGSAPFIPM 272
                                                                                                                                                                                                                                 279 TIISDEVYQENIFNDVKFHSM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHIZOBIACEAE; SINORHIZOBIUM
   9.18; 26.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L05064; G152149; -.
                                 Conservative
                                                                                                                                                                                                                                                                                                                     STANDARD;
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     RHIZOBIUM MELILOTI.
BACTERIA; PROTEOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91210178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-JJJC10
                                 54;
                                                                                                                                                                                                                                                                                                                    AATA_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                          219
                                                                                                                                               138
                                 Matches
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Length 400;

DB 1;

8.8%; Score 285;

Query Match

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                               24;
                                                                                                                                                                                                                                                                    :| :: : :| | : : :: | | :| | :| | PYKLSADDVFLTAGGTQAI-EVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRISTSTIUMLNVSTDPATFVQEALPKILENTKADFFKRIGLLKESSEICYREIKENKY 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTRQENNFKLKAEDLDRAITPKTKWFVFNSPSNPSGAAYSHEELKALTDVLMKHPHVWVL 202
                                                                                                                                                Gaps
                                                                                               31 RDVIGLGAGEPD-FDT-PDNIK-KAAIDAIDR-GETK-YTPVSGIPELREAIAKKFKREN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAT. GENET. 10:261-268(1995).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                             86 NLDYTAAQTIVGTGGKQILFNAFMATLN--PGDEVVIPAPYWVSYPEMVALCG-GTPVFV
                                                                                                                                                                                                                                                                                                                                                                                                          260 A-MDM-IQG-QQTS-GAASIAQWAAVEALNGPQ-DFIGRNKEIFQGRRDLVVSMLNQAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 IDDMYEHLTYGDFRFATPVEVEPGLYERILIMNGVSKAYAMTGWRIGYAA--GPLH-LIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISCP-TPEGAFYVYPSCAGLIGKTAPSGKVIETDEDFVSELLETEGVAVVHGSAFGLGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL AMINOTRANSFERASE YJL060W (EC 2.6.1..).
YJL060W OR J1138.
YJL060W OR J138.
YJ
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                               28:
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MURAKAMI Y., SASANUMA M., HAGIWARA H., SHIBATA T., OZAWA M., SASANUMA S., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K. YAMAZAKI M., TASHIRO H., EKI T., "Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.";
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
POHL T.M., ALJINOVIC G.;
SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
. No. 4.29e-33;
Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z49335; G1008205; -.
EMBL; D44603; G871966; -.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
   Pred.
86; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 FRISYATSEALLEEACRRIQRFC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQ
01-NOV-1997 (REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 VRITFACVPSSLQDGLERVKSFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 92-222 FROM N.A.
   Best Local Similarity 24.5%;
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YJG0_YEAST
P47039;
                                                                                                                                                                                                                                                                                                           138
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277 IVLLADEVY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 DGFDCEPSDIYLTSGASHAARLIMTLIIARPTDGVMVPAPQYPLYGAQIDLMSGSMVSYS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 PTL-LDHAEEKWFQNLFPTDV-VQRS-KMLLKESGSLGAYSASQGIPLVRRHVADFIRAR 156
                                                                                                                                                       184 WIIDFEQFEKAITSKTKAVIINTPHNPIGKVFTREELFTLGNICVKHNVVIISDEVYEHL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 VPYKLSADDVFLTAGGTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAAFNKLEVRHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSEENNWDIDFDQFKKSFDEASKKGINVRLCVVINPGNPTGACISENSMEKVLRFAKAKG
                                                                                                                                                                        01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WALSH S.V.;
                                   PYRIDOXAL PHOSPHATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 255; DB 1; Length 505;
Pred. No. 3.91e-27;
49; Mismatches 75; Indels 11;
                                                                                                                    э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRUVATE
                                                                                 Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
                                                                                 Score 258; DB 1; Length 444
Pred. No. 1.01e-27;
32; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.,
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: L-ALANINE + 2-OXOGLUTARATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL); 269909; E225673; -.
PFAM; PF00155; aminotran_1; 1.
HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
HYPOTHETICAL PROTEIN; AMINOTRANSFERASE; TRANSFERASE;
                                                                                                                                                                                                                        244 YF-TDSFTRIATLSPEIGQLTLTVGSAGKSFAATGWRIGWV 283
                                                                                                                                                                                                                                             263 VLGSAPFIPMGVFG-HIAPV-LSIGSLSKSWIVPGWRLGWV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8CD487CF CRC32;
                                                  444 AA; 50082 MW; 16A5EF3D CRC32
                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                              505
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 326 E
505 AA; 56627 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.9%;
Local Similarity 28.6%;
                                                                                 Query Match 8.0%;
Best Local Similarity 32.7%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRIDOXAL PHOSPHATE
                  PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                             LT 14
ALAT_SCHPO
Q10334;
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                                                  SEQUENCE
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Matches
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NAMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSQAASVAALNGPQDFLKERTESFQRRRNLVVNGLNA-IEGL-DCRVPEGAFYTFSGCAG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 VARRVIPSG-KRIESDIDFCAYLLEDSHVAVVPGSAFGLSPYFRISYATSEAELKEALER 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDFDTPDHVKQAASDAIHRGETK-YTALDGTPELKKAIREKFQRENGLAYEL--DEITVA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STDPATEVQEALPKILENTKADFFKRIIGLLKESSEICYREIKENKYITCP-HKPEGSMF 384
                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of a gene coding for a novel aspartate aminotransferase from Rhizobium meliloti.";
J. BACTERIOL. 175:4186-4196(1993).
-i. FUNCTION: INVOLVED IN SYMBIOTIC NITROGEN FIXATION.
-i. CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                      01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTARION UPDATE)
ASPARTATE AMINOTRANSFERASE B (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 TGAKQILFNAMMASL-D-PGDEVVIPTPYWTSYSDIVQICEGKPILIACDASSGFRLTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 RFVTPARLEPGLKDRTLTVNGVSKAYAMTGWRIGYAGG-PRALIKAMAVVQSQATSCPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLEAAITPRTRWVLLNSPSNPSGAAYSAADYRPLLDVLLKHPHVWLLVDDMYEHIVYDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRIDOXAL PHOSPHATE (BY SIMILARITY).
C72D06D6 CRC32;
                                                                                                                                                                                                                  RHIZOBIUM MELLICTI.
BACTERIA; PROTECBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.5%; Score 241; DB 1; Length 410; Best Local Similarity 21.0%; Pred. No. 2.09e-24; Matches 77; Conservative 100; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
                                                                                       410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 AA; 44453 MW;
                                                                                                                                                                                                                                                     RHIZOBIACEAE; SINORHIZOBIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L12149; G152151; -.
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                             STRAIN-104A14;
MEDLINE; 93308098.
ALFANO J.R., KAHN M.L.
|:::|||||
251 ILVIADEVY 259
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A40658;
                                                               15
TRHIME
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                                                                                     AATB_R
Q06191
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402 ISAACKR 408 : : | | 445 VKSFCQR 451

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Search completed: Fri Oct 1 13:50:38 1999 Job time : 20 secs.